SEQUENCE LISTING

<110> Guarente, Leonard P.
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    Cole, Francesca
    Kennedy, Brian

<120> GENES DETERMINING CELLULAR SENESCENCE IN
  YEAST

<130> 0050.1491-005

<150> US 08/396,001
<151> 1995-02-28

<150> PCT/US94/09351
<151> 1994-08-15

<150> US 08/107,408
<151> 1993-08-16

<150> US 09/323,433
<151> 1999-06-01

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gaaaaaagca gacaaaacaa aatttttcct ttttttcgcc tttgtttctc ctgattcggg 300
tatataagtg aataccatct a atg tgt ttc ctt ctc gag acc tcg gcg tct   351
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ccc aga tca aag ctc agc aaa gat ttt aaa ccg caa ttt acg ctc ctt   399
Pro Arg Ser Lys Leu Ser Lys Asp Phe Lys Pro Gln Phe Thr Leu Leu
             15   20   25

tca tcg gta act aag aag aaa aaa aaa aaa gta cga cca cac aat ttc   447
Ser Ser Val Thr Lys Lys Lys Lys Lys Lys Val Arg Pro His Asn Phe
          30   35   40

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cag tgt att cat tcc tta aac ttc gtt tat ttt tta ttc att cat tca    495
Gln Cys Ile His Ser Leu Asn Phe Val Tyr Phe Leu Phe Ile His Ser
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ttt tta ttt gaa tat aac caa cta cta gtc ctt cct tta aac aaa aat    543
Phe Leu Phe Glu Tyr Asn Gln Leu Leu Val Leu Pro Leu Asn Lys Asn
    60                  65                  70

tta ccc tcc ctt aat ttt tca aga aat tcc agt atg aaa tta tcc gct    591
Leu Pro Ser Leu Asn Phe Ser Arg Asn Ser Ser Met Lys Leu Ser Ala
75                  80                  85                  90

cta tta gct tta tca gcc tcc acc gcc gtc ttg gcc gct cca gct gtc    639
Leu Leu Ala Leu Ser Ala Ser Thr Ala Val Leu Ala Ala Pro Ala Val
                95                  100                 105

cac cat agt gac aac cac cac cac aac gac aag cgt gcc gtt gtc acc    687
His His Ser Asp Asn His His His Asn Asp Lys Arg Ala Val Val Thr
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gtt act cag tac gtc aac gca gac ggc gct gtt gtt att cca gct gcc    735
Val Thr Gln Tyr Val Asn Ala Asp Gly Ala Val Val Ile Pro Ala Ala
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acc acc gct acc tcg gcg gct gct gat gga aag gtc gag tct gtt gct    783
Thr Thr Ala Thr Ser Ala Ala Ala Asp Gly Lys Val Glu Ser Val Ala
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gct gcc acc act act ttg tcc tcg act gcc gcc gcc gct act acc tct    831
Ala Ala Thr Thr Thr Leu Ser Ser Thr Ala Ala Ala Ala Thr Thr Ser
155                 160                 165                 170

gcc gcc gcc tct tct tcc tcc tct tcc tct tcc tcc tct tcc tct tct    879
Ala Ala Ala Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
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tcc tct gtt ggt tct gga gat ttt gaa gat ggt acc att tcc tgt tct    927
Ser Ser Val Gly Ser Gly Asp Phe Glu Asp Gly Thr Ile Ser Cys Ser
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gat ttc cca tcc gga caa ggt gct gtc tcc ttg gac tgg tta ggt cta    975
Asp Phe Pro Ser Gly Gln Gly Ala Val Ser Leu Asp Trp Leu Gly Leu
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ggc ggc tgg gct tcc atc atg gac atg aac ggt aac acc gcc acc tct    1023
Gly Gly Trp Ala Ser Ile Met Asp Met Asn Gly Asn Thr Ala Thr Ser
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tgt caa gac gga tac tac tgt tct tac gct tgt tct cca ggt tac gct    1071
Cys Gln Asp Gly Tyr Tyr Cys Ser Tyr Ala Cys Ser Pro Gly Tyr Ala
235                 240                 245                 250

aag acc caa tgg cct tct gaa caa cct tcc gat ggt aga tcc gtt ggt    1119
Lys Thr Gln Trp Pro Ser Glu Gln Pro Ser Asp Gly Arg Ser Val Gly
            255                 260                 265

ggt tta tac tgt aag aac ggt aaa tta tac cgt tcc aac acc gac act    1167
Gly Leu Tyr Cys Lys Asn Gly Lys Leu Tyr Arg Ser Asn Thr Asp Thr
            270                 275                 280
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aac agt ttg tgt gta gaa ggt caa ggc tct gct caa gct gtt aac aag    1215
Asn Ser Leu Cys Val Glu Gly Gln Gly Ser Ala Gln Ala Val Asn Lys
        285                 290                 295

gtc tcc ggc tcc att gct atc tgt ggt acc gat tat cca ggt tct gaa    1263
Val Ser Gly Ser Ile Ala Ile Cys Gly Thr Asp Tyr Pro Gly Ser Glu
        300                 305                 310

aac atg gtc gtt cct acc gta gtt ggc gct ggt tcc tcc caa cca atc    1311
Asn Met Val Val Pro Thr Val Val Gly Ala Gly Ser Ser Gln Pro Ile
315                 320                 325                 330

aac gtc atc aag gag gac tcc tac tat caa tgg caa ggt aag aag acc    1359
Asn Val Ile Lys Glu Asp Ser Tyr Tyr Gln Trp Gln Gly Lys Lys Thr
                335                 340                 345

tct gcc caa tac tac gtt aac aac gct ggt gtc tct gtg gaa gat ggt    1407
Ser Ala Gln Tyr Tyr Val Asn Asn Ala Gly Val Ser Val Glu Asp Gly
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tgt atc tgg ggt act gag ggt tcc ggt gtc ggt aac tgg gcc cca gtt    1455
Cys Ile Trp Gly Thr Glu Gly Ser Gly Val Gly Asn Trp Ala Pro Val
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gtc ttg ggt gct ggt tac act gat ggt atc act tac ttg tcc atc att    1503
Val Leu Gly Ala Gly Tyr Thr Asp Gly Ile Thr Tyr Leu Ser Ile Ile
        380                 385                 390

cca aac cca aac aac aaa gaa gca cca aac ttt aac atc aag atc gtt    1551
Pro Asn Pro Asn Asn Lys Glu Ala Pro Asn Phe Asn Ile Lys Ile Val
395                 400                 405                 410

gcc acc gat ggc tct acc gtc aat ggt gct tgc tct tac gaa aat ggt    1599
Ala Thr Asp Gly Ser Thr Val Asn Gly Ala Cys Ser Tyr Glu Asn Gly
                415                 420                 425

gtc tac tct ggc tct ggc tct gac ggt tgt act gtt tca gtt act tct    1647
Val Tyr Ser Gly Ser Gly Ser Asp Gly Cys Thr Val Ser Val Thr Ser
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ggt tct gct aac ttt gtc ttc tac taggcctttt ttccttgaat attgcaaata   1701
Gly Ser Ala Asn Phe Val Phe Tyr
                445                 450

agcttttgct agtacttttt ttactccgtt cattttatgg tttatttttc aattagttcg  1761
ttttccaca atacaaaaaa acacagtcct ttgtactatc ccttttattt cattattttt   1821
tcttttttaa gataccacta gatattatca tatatagcat attatataac ataaaaagtc  1881
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Lys Lys Lys Lys Val Arg Pro His Asn Phe Gln Cys Ile His Ser Leu
        35   40   45
Asn Phe Val Tyr Phe Leu Phe Ile His Ser Phe Leu Phe Glu Tyr Asn
    50   55   60
Gln Leu Leu Val Leu Pro Leu Asn Lys Asn Leu Pro Ser Leu Asn Phe
65   70   75   80
Ser Arg Asn Ser Ser Met Lys Leu Ser Ala Leu Leu Ala Leu Ser Ala
                85   90   95
Ser Thr Ala Val Leu Ala Ala Pro Ala Val His His Ser Asp Asn His
            100   105   110
His His Asn Asp Lys Arg Ala Val Val Thr Val Thr Gln Tyr Val Asn
    115   120   125
Ala Asp Gly Ala Val Val Ile Pro Ala Ala Thr Thr Ala Thr Ser Ala
    130   135   140
Ala Ala Asp Gly Lys Val Glu Ser Val Ala Ala Ala Thr Thr Thr Leu
145   150   155   160
Ser Ser Thr Ala Ala Ala Ala Thr Thr Ser Ala Ala Ala Ser Ser Ser
            165   170   175
Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Val Gly Ser Gly
            180   185   190
Asp Phe Glu Asp Gly Thr Ile Ser Cys Ser Asp Phe Pro Ser Gly Gln
            195   200   205
Gly Ala Val Ser Leu Asp Trp Leu Gly Leu Gly Gly Trp Ala Ser Ile
    210   215   220
Met Asp Met Asn Gly Asn Thr Ala Thr Ser Cys Gln Asp Gly Tyr Tyr
225   230   235   240
Cys Ser Tyr Ala Cys Ser Pro Gly Tyr Ala Lys Thr Gln Trp Pro Ser
            245   250   255
Glu Gln Pro Ser Asp Gly Arg Ser Val Gly Gly Leu Tyr Cys Lys Asn
            260   265   270
Gly Lys Leu Tyr Arg Ser Asn Thr Asp Thr Asn Ser Leu Cys Val Glu
    275   280   285
Gly Gln Gly Ser Ala Gln Ala Val Asn Lys Val Ser Gly Ser Ile Ala
    290   295   300
Ile Cys Gly Thr Asp Tyr Pro Gly Ser Glu Asn Met Val Val Pro Thr
305   310   315   320
Val Val Gly Ala Gly Ser Ser Gln Pro Ile Asn Val Ile Lys Glu Asp
            325   330   335
Ser Tyr Tyr Gln Trp Gln Gly Lys Lys Thr Ser Ala Gln Tyr Tyr Val
            340   345   350
Asn Asn Ala Gly Val Ser Val Glu Asp Gly Cys Ile Trp Gly Thr Glu
    355   360   365
Gly Ser Gly Val Gly Asn Trp Ala Pro Val Val Leu Gly Ala Gly Tyr
    370   375   380
Thr Asp Gly Ile Thr Tyr Leu Ser Ile Ile Pro Asn Pro Asn Asn Lys
385   390   395   400
Glu Ala Pro Asn Phe Asn Ile Lys Ile Val Ala Thr Asp Gly Ser Thr
            405   410   415
Val Asn Gly Ala Cys Ser Tyr Glu Asn Gly Val Tyr Ser Gly Ser Gly
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agggcttcgg gaaagaggcg cctcaggcaa aaatgagcaa aaaaaaaaa aaaaagaaaa 240
gattcgaaga tctatgaaaa atttatgcag attcgttgag agttataagg attttactct 300
ttatggttat aggtttcatt ctaaaatcaa gcataaattt tgtgttttgt cttcctcttt 360
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ttatttttgt ggtttcactt tactaacaca acattctttt attcaatcag atcaataacg 600
aaccatttcc atctgccgac tcagcatcga ttttaactac gtctacatca ataactcct 660
ta atg tct tac aat cat cag cct caa cta tct att aac tcc gtc caa    707
   Met Ser Tyr Asn His Gln Pro Gln Leu Ser Ile Asn Ser Val Gln
    1               5                  10                  15

tca ctc ttg gag ccc gtg acc cct ccg cct ttg ggc cag atg aat aac    755
Ser Leu Leu Glu Pro Val Thr Pro Pro Pro Leu Gly Gln Met Asn Asn
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aaa aga aac cat caa aag gct cat tcg ctt gat ctc tct ggt ttt aat    803
Lys Arg Asn His Gln Lys Ala His Ser Leu Asp Leu Ser Gly Phe Asn
            35                  40                  45

cag ttc ata tca tcg aca caa tct ccc ttg gct ttg atg aat aat aca    851
Gln Phe Ile Ser Ser Thr Gln Ser Pro Leu Ala Leu Met Asn Asn Thr
        50                  55                  60

tca aca tcg aat tct gct aac tct ttt tcc ccg aat cct aat gct gct    899
Ser Thr Ser Asn Ser Ala Asn Ser Phe Ser Pro Asn Pro Asn Ala Ala
    65                  70                  75

agc aac tcc act ggg ctt tca gcc tca atg gca aat cct cca gcc att    947
Ser Asn Ser Thr Gly Leu Ser Ala Ser Met Ala Asn Pro Pro Ala Ile
 80                  85                  90                  95

cta cca tta atc aat gag ttt gat ctg gaa atg gat ggt ccc agg aga    995
Leu Pro Leu Ile Asn Glu Phe Asp Leu Glu Met Asp Gly Pro Arg Arg
                100                 105                 110

aaa tca agc cac gat ttc acg gtt gtt gct cct tcg aac tct ggt gtc    1043
Lys Ser Ser His Asp Phe Thr Val Val Ala Pro Ser Asn Ser Gly Val
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aat acc tcc agt tta att atg gaa aca cca tcc tct tca gtg act cct    1091
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Asn Thr Ser Ser Leu Ile Met Glu Thr Pro Ser Ser Ser Val Thr Pro
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gct gca tct ctc aga aat ttt agc aat agt aat aat gct gct tcc aaa    1139
Ala Ala Ser Leu Arg Asn Phe Ser Asn Ser Asn Asn Ala Ala Ser Lys
    145                 150                 155

tgt gga gtg gat aat tcg tca ttt ggt ttg agt agc tca acg tct tca    1187
Cys Gly Val Asp Asn Ser Ser Phe Gly Leu Ser Ser Ser Thr Ser Ser
160                 165                 170                 175

tct atg gtc gaa atc agc gca cta ccc ctt aga gat ctg gat tat atc    1235
Ser Met Val Glu Ile Ser Ala Leu Pro Leu Arg Asp Leu Asp Tyr Ile
            180                 185                 190

aaa ctt gcc act gac cag ttt ggc tgc cgt ttt ctt caa aaa aaa tta    1283
Lys Leu Ala Thr Asp Gln Phe Gly Cys Arg Phe Leu Gln Lys Lys Leu
            195                 200                 205

gaa acc ccc agt gaa tcc aat atg gtg aga gac ttg atg tat gaa caa    1331
Glu Thr Pro Ser Glu Ser Asn Met Val Arg Asp Leu Met Tyr Glu Gln
            210                 215                 220

att aag cca ttt ttc ttg gac ctt att ttg gat ccg ttc ggt aac tat    1379
Ile Lys Pro Phe Phe Leu Asp Leu Ile Leu Asp Pro Phe Gly Asn Tyr
            225                 230                 235

ttg gtt caa aaa cta tgc gat tat tta act gcc gag caa aag aca tta    1427
Leu Val Gln Lys Leu Cys Asp Tyr Leu Thr Ala Glu Gln Lys Thr Leu
240                 245                 250                 255

tta ata caa aca ata tat cca aat gtt ttc caa ata tca atc aat cag    1475
Leu Ile Gln Thr Ile Tyr Pro Asn Val Phe Gln Ile Ser Ile Asn Gln
            260                 265                 270

tac gga act cgt tcc tta cag aaa att ata gac act gtc gat aac gaa    1523
Tyr Gly Thr Arg Ser Leu Gln Lys Ile Ile Asp Thr Val Asp Asn Glu
            275                 280                 285

gtt caa atc gat ctc att att aag gga ttt tcc caa gaa ttt act tcg    1571
Val Gln Ile Asp Leu Ile Ile Lys Gly Phe Ser Gln Glu Phe Thr Ser
            290                 295                 300

att gag caa gtg gtt act ttg ata aac gat ctt aat ggt aac cat gtg    1619
Ile Glu Gln Val Val Thr Leu Ile Asn Asp Leu Asn Gly Asn His Val
            305                 310                 315

att caa aag tgt att ttc aaa ttc tcg cca tca aaa ttt ggt ttc atc    1667
Ile Gln Lys Cys Ile Phe Lys Phe Ser Pro Ser Lys Phe Gly Phe Ile
320                 325                 330                 335

ata gat gct att gta gaa caa aat aat atc att acc att tct acc cat    1715
Ile Asp Ala Ile Val Glu Gln Asn Asn Ile Ile Thr Ile Ser Thr His
            340                 345                 350

aaa cat ggt tgt tgc gta cta caa aaa tta cta agc gtt tgt act cta    1763
Lys His Gly Cys Cys Val Leu Gln Lys Leu Leu Ser Val Cys Thr Leu
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tta atc aac gat cag ttc ggt aat tat atc atc caa ttt ctg tta gat     1859
Leu Ile Asn Asp Gln Phe Gly Asn Tyr Ile Ile Gln Phe Leu Leu Asp
        385                 390                 395

atc aaa gaa ttg gac ttt tac tta ttg gct gag tta ttt aac cgt tta     1907
Ile Lys Glu Leu Asp Phe Tyr Leu Leu Ala Glu Leu Phe Asn Arg Leu
400                 405                 410                 415

tcc aat gaa tta tgt caa cta tct tgt ttg aag ttc tcc tca aat gtt     1955
Ser Asn Glu Leu Cys Gln Leu Ser Cys Leu Lys Phe Ser Ser Asn Val
                420                 425                 430

gtg gaa aaa ttc att aaa aaa tta ttt aga atc att act gga ttt att     2003
Val Glu Lys Phe Ile Lys Lys Leu Phe Arg Ile Ile Thr Gly Phe Ile
                435                 440                 445

gtt aat aac aat ggg ggt gcc tcc caa agg act gca gtt gct tct gat     2051
Val Asn Asn Asn Gly Gly Ala Ser Gln Arg Thr Ala Val Ala Ser Asp
                450                 455                 460

gac gtg att aat gct tct atg aac att ctt ttg act acc att gat ata     2099
Asp Val Ile Asn Ala Ser Met Asn Ile Leu Leu Thr Thr Ile Asp Ile
                465                 470                 475

ttc aca gtc aat tta aat gtg cta atc agg gat aat ttt ggt aat tat     2147
Phe Thr Val Asn Leu Asn Val Leu Ile Arg Asp Asn Phe Gly Asn Tyr
480                 485                 490                 495

gcg tta caa acg cta tta gac gtt aag aat tat tct cct ctg ctt gct     2195
Ala Leu Gln Thr Leu Leu Asp Val Lys Asn Tyr Ser Pro Leu Leu Ala
                500                 505                 510

tac aac aaa aat agt aac gca att ggg caa aac agc tct agt aca ttg     2243
Tyr Asn Lys Asn Ser Asn Ala Ile Gly Gln Asn Ser Ser Ser Thr Leu
                515                 520                 525

aat tac ggt aac ttt tgt aac gat ttt tca ttg aaa att ggt aac ttg     2291
Asn Tyr Gly Asn Phe Cys Asn Asp Phe Ser Leu Lys Ile Gly Asn Leu
                530                 535                 540

att gtc ctt aca aaa gaa tta ctt cca agt att aaa act aca tcc tat     2339
Ile Val Leu Thr Lys Glu Leu Leu Pro Ser Ile Lys Thr Thr Ser Tyr
        545                 550                 555

gca aag aaa att aag ttg aaa gtt aaa gct tat gca gaa gcc aca ggt     2387
Ala Lys Lys Ile Lys Leu Lys Val Lys Ala Tyr Ala Glu Ala Thr Gly
560                 565                 570                 575

ata cca ttc act gac ata tct cct caa gtc act gca atg agt cat aac     2435
Ile Pro Phe Thr Asp Ile Ser Pro Gln Val Thr Ala Met Ser His Asn
                580                 585                 590

aat ctt caa acg att aac aac gaa aat aag aac ccc cat aac aaa aat     2483
Asn Leu Gln Thr Ile Asn Asn Glu Asn Lys Asn Pro His Asn Lys Asn
                595                 600                 605
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agt cat aat cat aat cat aat cat aat cat aac cat gct cac aat aat    2531
Ser His Asn His Asn His Asn His Asn His Asn His Ala His Asn Asn
        610             615                 620

aat aac aat aat aat caa aag agt cat acc cgt cat ttt tct tta cca    2579
Asn Asn Asn Asn Asn Gln Lys Ser His Thr Arg His Phe Ser Leu Pro
        625             630                 635

gct aat gct tac cat aga aga agt aac agc tct gta acc aat aat ttc    2627
Ala Asn Ala Tyr His Arg Arg Ser Asn Ser Ser Val Thr Asn Asn Phe
640             645                 650                 655

tca aac caa tat gca caa gat cag aaa att cac tct ccg caa caa att    2675
Ser Asn Gln Tyr Ala Gln Asp Gln Lys Ile His Ser Pro Gln Gln Ile
                660             665                 670

atg aac ttc aac caa aac gca tat ccc tcg atg gga gca cct tct ttc    2723
Met Asn Phe Asn Gln Asn Ala Tyr Pro Ser Met Gly Ala Pro Ser Phe
            675                 680                 685

aat tct caa act aac cca cca ttg gta agc cat aac tcg tta caa aac    2771
Asn Ser Gln Thr Asn Pro Pro Leu Val Ser His Asn Ser Leu Gln Asn
            690                 695                 700

ttc gac aac cgc cag ttt gca aat tta atg gca cat cct aat tct gct    2819
Phe Asp Asn Arg Gln Phe Ala Asn Leu Met Ala His Pro Asn Ser Ala
        705                 710                 715

gca cca atc cat tcg ttc tca tca tct aac att acc aat gtg aat cct    2867
Ala Pro Ile His Ser Phe Ser Ser Ser Asn Ile Thr Asn Val Asn Pro
720                 725                 730                 735

aat gtt tca agg gga ttt aag cag cct gga ttt atg atg aat gaa acc    2915
Asn Val Ser Arg Gly Phe Lys Gln Pro Gly Phe Met Met Asn Glu Thr
            740                 745                 750

gac aaa att aat gct aat cac ttc tcg cca tac tct aat gca aat agt    2963
Asp Lys Ile Asn Ala Asn His Phe Ser Pro Tyr Ser Asn Ala Asn Ser
        755                 760                 765

caa aac ttc aat gaa tct ttt gtg cct cgt atg caa tat caa acg gaa    3011
Gln Asn Phe Asn Glu Ser Phe Val Pro Arg Met Gln Tyr Gln Thr Glu
        770                 775                 780

ggt gca aac tgg gat tca agt ttg tca atg aag tcg cag cat att ggt    3059
Gly Ala Asn Trp Asp Ser Ser Leu Ser Met Lys Ser Gln His Ile Gly
        785                 790                 795

caa ggc cca tat aat caa gtt aat atg agc cgc aac gct agt att tcc    3107
Gln Gly Pro Tyr Asn Gln Val Asn Met Ser Arg Asn Ala Ser Ile Ser
800                 805                 810                 815

aat atg cct gcc atg aat acc gct aga aca tct gat gaa ctt caa ttc    3155
Asn Met Pro Ala Met Asn Thr Ala Arg Thr Ser Asp Glu Leu Gln Phe
                820             825                 830

act ttg cca taatactttt ttttctttct ttttctttcc ttcttactgt          3204
Thr Leu Pro
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acaaatattt tacgcagaaa tcaaagacaa aagaaaaata aaaaataaaa aataaaaaat 3264
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gcaaactatt gccatcttta tattttgtat tctgtttccg aacacgtatc caaaatcctc 3384
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            20                  25                  30
Arg Asn His Gln Lys Ala His Ser Leu Asp Leu Ser Gly Phe Asn Gln
        35                  40                  45
Phe Ile Ser Ser Thr Gln Ser Pro Leu Ala Leu Met Asn Asn Thr Ser
    50                  55                  60
Thr Ser Asn Ser Ala Asn Ser Phe Ser Pro Asn Pro Asn Ala Ala Ser
65                  70                  75                  80
Asn Ser Thr Gly Leu Ser Ala Ser Met Ala Asn Pro Pro Ala Ile Leu
                85                  90                  95
Pro Leu Ile Asn Glu Phe Asp Leu Glu Met Asp Gly Pro Arg Arg Lys
            100                 105                 110
Ser Ser His Asp Phe Thr Val Val Ala Pro Ser Asn Ser Gly Val Asn
        115                 120                 125
Thr Ser Ser Leu Ile Met Glu Thr Pro Ser Ser Ser Val Thr Pro Ala
    130                 135                 140
Ala Ser Leu Arg Asn Phe Ser Asn Ser Asn Asn Ala Ala Ser Lys Cys
145                 150                 155                 160
Gly Val Asp Asn Ser Ser Phe Gly Leu Ser Ser Ser Thr Ser Ser Ser
                165                 170                 175
Met Val Glu Ile Ser Ala Leu Pro Leu Arg Asp Leu Asp Tyr Ile Lys
            180                 185                 190
Leu Ala Thr Asp Gln Phe Gly Cys Arg Phe Leu Gln Lys Lys Leu Glu
        195                 200                 205
Thr Pro Ser Glu Ser Asn Met Val Arg Asp Leu Met Tyr Glu Gln Ile
    210                 215                 220
Lys Pro Phe Phe Leu Asp Leu Ile Leu Asp Pro Phe Gly Asn Tyr Leu
225                 230                 235                 240
Val Gln Lys Leu Cys Asp Tyr Leu Thr Ala Glu Gln Lys Thr Leu Leu
                245                 250                 255
Ile Gln Thr Ile Tyr Pro Asn Val Phe Gln Ile Ser Ile Asn Gln Tyr
            260                 265                 270
Gly Thr Arg Ser Leu Gln Lys Ile Ile Asp Thr Val Asp Asn Glu Val
        275                 280                 285
Gln Ile Asp Leu Ile Ile Lys Gly Phe Ser Gln Glu Phe Thr Ser Ile
    290                 295                 300
Glu Gln Val Val Thr Leu Ile Asn Asp Leu Asn Gly Asn His Val Ile
305                 310                 315                 320
Gln Lys Cys Ile Phe Lys Phe Ser Pro Ser Lys Phe Gly Phe Ile Ile
                325                 330                 335
Asp Ala Ile Val Glu Gln Asn Asn Ile Ile Thr Ile Ser Thr His Lys
            340                 345                 350
His Gly Cys Cys Val Leu Gln Lys Leu Leu Ser Val Cys Thr Leu Gln
        355                 360                 365
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Gln Ile Phe Lys Ile Ser Val Lys Ile Val Gln Phe Leu Pro Gly Leu
    370             375             380
Ile Asn Asp Gln Phe Gly Asn Tyr Ile Ile Gln Phe Leu Leu Asp Ile
385             390             395             400
Lys Glu Leu Asp Phe Tyr Leu Leu Ala Glu Leu Phe Asn Arg Leu Ser
            405             410             415
Asn Glu Leu Cys Gln Leu Ser Cys Leu Lys Phe Ser Ser Asn Val Val
            420             425             430
Glu Lys Phe Ile Lys Lys Leu Phe Arg Ile Ile Thr Gly Phe Ile Val
        435             440             445
Asn Asn Asn Gly Gly Ala Ser Gln Arg Thr Ala Val Ala Ser Asp Asp
        450             455             460
Val Ile Asn Ala Ser Met Asn Ile Leu Leu Thr Thr Ile Asp Ile Phe
465             470             475             480
Thr Val Asn Leu Asn Val Leu Ile Arg Asp Asn Phe Gly Asn Tyr Ala
            485             490             495
Leu Gln Thr Leu Leu Asp Val Lys Asn Tyr Ser Pro Leu Leu Ala Tyr
            500             505             510
Asn Lys Asn Ser Asn Ala Ile Gly Gln Asn Ser Ser Ser Thr Leu Asn
        515             520             525
Tyr Gly Asn Phe Cys Asn Asp Phe Ser Leu Lys Ile Gly Asn Leu Ile
        530             535             540
Val Leu Thr Lys Glu Leu Leu Pro Ser Ile Lys Thr Thr Ser Tyr Ala
545             550             555             560
Lys Lys Ile Lys Leu Lys Val Lys Ala Tyr Ala Glu Ala Thr Gly Ile
            565             570             575
Pro Phe Thr Asp Ile Ser Pro Gln Val Thr Ala Met Ser His Asn Asn
            580             585             590
Leu Gln Thr Ile Asn Asn Glu Asn Lys Asn Pro His Asn Lys Asn Ser
        595             600             605
His Asn His Asn His Asn His Asn His Asn His Ala His Asn Asn Asn
    610             615             620
Asn Asn Asn Asn Gln Lys Ser His Thr Arg His Phe Ser Leu Pro Ala
625             630             635             640
Asn Ala Tyr His Arg Arg Ser Asn Ser Ser Val Thr Asn Asn Phe Ser
            645             650             655
Asn Gln Tyr Ala Gln Asp Gln Lys Ile His Ser Pro Gln Gln Ile Met
            660             665             670
Asn Phe Asn Gln Asn Ala Tyr Pro Ser Met Gly Ala Pro Ser Phe Asn
    675             680             685
Ser Gln Thr Asn Pro Pro Leu Val Ser His Asn Ser Leu Gln Asn Phe
    690             695             700
Asp Asn Arg Gln Phe Ala Asn Leu Met Ala His Pro Asn Ser Ala Ala
705             710             715             720
Pro Ile His Ser Phe Ser Ser Ser Asn Ile Thr Asn Val Asn Pro Asn
            725             730             735
Val Ser Arg Gly Phe Lys Gln Pro Gly Phe Met Met Asn Glu Thr Asp
            740             745             750
Lys Ile Asn Ala Asn His Phe Ser Pro Tyr Ser Asn Ala Asn Ser Gln
    755             760             765
Asn Phe Asn Glu Ser Phe Val Pro Arg Met Gln Tyr Gln Thr Glu Gly
    770             775             780
Ala Asn Trp Asp Ser Ser Leu Ser Met Lys Ser Gln His Ile Gly Gln
785             790             795             800
Gly Pro Tyr Asn Gln Val Asn Met Ser Arg Asn Ala Ser Ile Ser Asn
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Met Pro Ala Met Asn Thr Ala Arg Thr Ser Asp Glu Leu Gln Phe Thr
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Leu Pro
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ctttgtgact gcaaatttta atttgtgacg ccttttctta ttactcatgt atttgtcact 180
cttgacgatt gtttttttc tatatttttt ttgttctggg gtcctccaga gaataaaaaa 240
taatgatcaa tatagtagat agtatagtta tattcttatt cgttgcacct tgtttaacaa 300
atcactcaga ctcaaagaga atatcggttg gttatctctc tccgaaggtg aacagcaaac 360
agtacctcac gtctttttt tgaatagttt ttttttttgt tgaaacagaa aaaaaacttt 420
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gagccgtcat taatattatt cgtttttgta cactattcca gacgatttat ttttagtaca 540
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ctttaggttc ttttaagagt ctctgttcat tttccgttct tactgtttct ttgtcctcga 660
tatctttttaa gaaagagaga actaagcgct gtaacatttt taagtggacc tacgtt atg 719
                                                                  Met
                                                                  1
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tct aca aaa ggt ttg aaa gaa gaa atc gat gat gta cca tca gta gac     767
Ser Thr Lys Gly Leu Lys Glu Glu Ile Asp Asp Val Pro Ser Val Asp
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cct gtc gtt tca gaa aca gtc aat tct gct tta gag cag ttg caa cta     815
Pro Val Val Ser Glu Thr Val Asn Ser Ala Leu Glu Gln Leu Gln Leu
        20                  25                  30

gat gat cca gag gaa aac gcc acc tct aat gca ttt gcg aat aaa gtt     863
Asp Asp Pro Glu Glu Asn Ala Thr Ser Asn Ala Phe Ala Asn Lys Val
    35                  40                  45

tct caa gat tct caa ttc gct aat ggc cct ccg tcg caa atg ttt cca     911
Ser Gln Asp Ser Gln Phe Ala Asn Gly Pro Pro Ser Gln Met Phe Pro
50                  55                  60                  65

cat cca caa atg atg ggt gga atg ggc ttc atg ccc tac tct caa atg     959
His Pro Gln Met Met Gly Gly Met Gly Phe Met Pro Tyr Ser Gln Met
                70                  75                  80

atg cag gtt cct cat aat cct tgt cca ttt ttt ccg ccc cct gat ttt     1007
Met Gln Val Pro His Asn Pro Cys Pro Phe Phe Pro Pro Pro Asp Phe
                85                  90                  95

aat gat cca aca gca cca ttg agt agc tcg ccc ttg aat gca ggc ggt     1055
Asn Asp Pro Thr Ala Pro Leu Ser Ser Ser Pro Leu Asn Ala Gly Gly
            100                 105                 110

cca cca atg tta ttc aag aat gac tca ctt cca ttt caa atg ctg tct     1103
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            Pro Pro Met Leu Phe Lys Asn Asp Ser Leu Pro Phe Gln Met Leu Ser
                115                 120                 125

tcg ggt gct gcg gta gca act caa ggt gga caa aat cta aac cca ttg        1151
Ser Gly Ala Ala Val Ala Thr Gln Gly Gly Gln Asn Leu Asn Pro Leu
130                 135                 140                 145

ata aat gac aat tca atg aag gta ttg cca atc gca tcg gct gat ccg        1199
Ile Asn Asp Asn Ser Met Lys Val Leu Pro Ile Ala Ser Ala Asp Pro
                150                 155                 160

tta tgg act cat tca aac gta cca gga tca gca tct gta gcc att gaa        1247
Leu Trp Thr His Ser Asn Val Pro Gly Ser Ala Ser Val Ala Ile Glu
                165                 170                 175

gaa acc acc gct act cta caa gaa agc cta cca tct aag ggc agg gag        1295
Glu Thr Thr Ala Thr Leu Gln Glu Ser Leu Pro Ser Lys Gly Arg Glu
                180                 185                 190

tct aat aat aag gct agt tcg ttc aga aga caa act ttt cat gct tta        1343
Ser Asn Asn Lys Ala Ser Ser Phe Arg Arg Gln Thr Phe His Ala Leu
                195                 200                 205

tca cca act gac ctt atc aat gcg gcc aac aat gta acc ttg tca aag        1391
Ser Pro Thr Asp Leu Ile Asn Ala Ala Asn Asn Val Thr Leu Ser Lys
210                 215                 220                 225

gac ttc caa tct gac atg cag aat ttt tct aag gct aag aaa ccg tct        1439
Asp Phe Gln Ser Asp Met Gln Asn Phe Ser Lys Ala Lys Lys Pro Ser
                230                 235                 240

gta gga gct aac aat act gca aaa acc aga act caa tcc ata tct ttt        1487
Val Gly Ala Asn Asn Thr Ala Lys Thr Arg Thr Gln Ser Ile Ser Phe
                245                 250                 255

gat aat act ccc tcc tca acg tca ttt ata ccc cca acc aat agt gtt        1535
Asp Asn Thr Pro Ser Ser Thr Ser Phe Ile Pro Pro Thr Asn Ser Val
                260                 265                 270

tct gag aaa tta tcc gat ttc aaa ata gaa acc tcg aag gag gat ttg        1583
Ser Glu Lys Leu Ser Asp Phe Lys Ile Glu Thr Ser Lys Glu Asp Leu
                275                 280                 285

att aat aaa act gca cca gct aaa aaa gag agt cct aca act tat ggt        1631
Ile Asn Lys Thr Ala Pro Ala Lys Lys Glu Ser Pro Thr Thr Tyr Gly
290                 295                 300                 305

gca gca tat cca tat ggg gga cct tta ctt caa cca aat cct att atg        1679
Ala Ala Tyr Pro Tyr Gly Gly Pro Leu Leu Gln Pro Asn Pro Ile Met
                310                 315                 320

cca ggc cac cca cat aat ata tcc tcc cct atc tat ggt att aga tca        1727
Pro Gly His Pro His Asn Ile Ser Ser Pro Ile Tyr Gly Ile Arg Ser
                325                 330                 335

cct ttt cct aat tct tat gaa atg ggc gcg caa ttt caa cct ttc tct        1775
Pro Phe Pro Asn Ser Tyr Glu Met Gly Ala Gln Phe Gln Pro Phe Ser
                340                 345                 350
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ccg att tta aat cct acg agt cat tca cta aat gca aat tct cca att    1823
Pro Ile Leu Asn Pro Thr Ser His Ser Leu Asn Ala Asn Ser Pro Ile
    355                 360                 365

cct cta acc caa tcg cca att cat ctt gca cca gtt tta aac cct agt    1871
Pro Leu Thr Gln Ser Pro Ile His Leu Ala Pro Val Leu Asn Pro Ser
370                 375                 380                 385

tca aat tct gtt gcc ttt tca gat atg aag aat gat ggt ggt aag ccc    1919
Ser Asn Ser Val Ala Phe Ser Asp Met Lys Asn Asp Gly Gly Lys Pro
                390                 395                 400

acc acc gat aac gac aag gcg ggt cca aat gtt agg atg gat tta ata    1967
Thr Thr Asp Asn Asp Lys Ala Gly Pro Asn Val Arg Met Asp Leu Ile
            405                 410                 415

aat cct aat ctt ggg cca tca atg caa cct ttc cac ata tta cct ccc    2015
Asn Pro Asn Leu Gly Pro Ser Met Gln Pro Phe His Ile Leu Pro Pro
            420                 425                 430

cag caa aac acc ccc cct cct ccc tgg ctt tat agc act cca cct ccc    2063
Gln Gln Asn Thr Pro Pro Pro Pro Trp Leu Tyr Ser Thr Pro Pro Pro
        435                 440                 445

ttc aac gca atg gtt ccg cct cat ttg ttg gct caa aat cat atg ccg    2111
Phe Asn Ala Met Val Pro Pro His Leu Leu Ala Gln Asn His Met Pro
450                 455                 460                 465

tta atg aat agc gcc aat aat aaa cat cat ggt cgt aat aac aat agc    2159
Leu Met Asn Ser Ala Asn Asn Lys His His Gly Arg Asn Asn Asn Ser
                470                 475                 480

atg tca agt cat aat gac aat gac aac att ggt aat tct aat tac aac    2207
Met Ser Ser His Asn Asp Asn Asp Asn Ile Gly Asn Ser Asn Tyr Asn
            485                 490                 495

aat aaa gac aca ggt cgt tct aac gtt ggt aaa atg aaa aat atg aaa    2255
Asn Lys Asp Thr Gly Arg Ser Asn Val Gly Lys Met Lys Asn Met Lys
        500                 505                 510

aac agt tat cat ggc tac tat aat aac aat aat aat aat aat aat aat    2303
Asn Ser Tyr His Gly Tyr Tyr Asn Asn Asn Asn Asn Asn Asn Asn Asn
        515                 520                 525

aac aat aat aat aat aac agt aat gct acc aac agc aac agc gcg gaa    2351
Asn Asn Asn Asn Asn Asn Ser Asn Ala Thr Asn Ser Asn Ser Ala Glu
530                 535                 540                 545

aaa caa cgt aaa att gag gag tcg tcg aga ttt gcg gac gca gtt tta    2399
Lys Gln Arg Lys Ile Glu Glu Ser Ser Arg Phe Ala Asp Ala Val Leu
            550                 555                 560

gac caa tat atc gga agt att cac tca ttg tgt aaa gac caa cat ggt    2447
Asp Gln Tyr Ile Gly Ser Ile His Ser Leu Cys Lys Asp Gln His Gly
            565                 570                 575

tgt cgt ttt ctg caa aag cag ttg gat att ctc ggc agt aag gcg gcg    2495
Cys Arg Phe Leu Gln Lys Gln Leu Asp Ile Leu Gly Ser Lys Ala Ala
        580                 585                 590
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gac cga att ttt gaa gaa act aag gat tat acg gtt gaa ttg atg act    2543
Asp Arg Ile Phe Glu Glu Thr Lys Asp Tyr Thr Val Glu Leu Met Thr
    595             600             605

gat tca ttc ggt aat tat ttg atc cag aag cta ttg gaa gag gtt acc    2591
Asp Ser Phe Gly Asn Tyr Leu Ile Gln Lys Leu Leu Glu Glu Val Thr
610             615             620             625

aca gaa caa aga atc gta ctc aca aaa ata tct tcc cct cat ttt gtc    2639
Thr Glu Gln Arg Ile Val Leu Thr Lys Ile Ser Ser Pro His Phe Val
            630             635             640

gaa att tcc tta aac cct cat ggt act agg gca tta caa aaa ctc att    2687
Glu Ile Ser Leu Asn Pro His Gly Thr Arg Ala Leu Gln Lys Leu Ile
            645             650             655

gaa tgc atc aaa aca gat gaa gaa gca cag att gtt gtt gat tct tta    2735
Glu Cys Ile Lys Thr Asp Glu Glu Ala Gln Ile Val Val Asp Ser Leu
        660             665             670

cgc cct tat act gtc cag ttg agt aag gat tta aat ggt aat cat gtt    2783
Arg Pro Tyr Thr Val Gln Leu Ser Lys Asp Leu Asn Gly Asn His Val
    675             680             685

att caa aaa tgt ttg caa agg ttg aag cct gaa aac ttc cag ttt atc    2831
Ile Gln Lys Cys Leu Gln Arg Leu Lys Pro Glu Asn Phe Gln Phe Ile
690             695             700             705

ttt gac gca atc tct gat agc tgt att gat att gct act cat aga cac    2879
Phe Asp Ala Ile Ser Asp Ser Cys Ile Asp Ile Ala Thr His Arg His
            710             715             720

ggg tgt tgc gtt ttg caa cgt tgt cta gat cat ggg act aca gaa caa    2927
Gly Cys Cys Val Leu Gln Arg Cys Leu Asp His Gly Thr Thr Glu Gln
        725             730             735

tgt gac aat ctg tgt gat aag ttg cta gcc ctt gtt gat aaa tta act    2975
Cys Asp Asn Leu Cys Asp Lys Leu Leu Ala Leu Val Asp Lys Leu Thr
        740             745             750

ttg gat cca ttt ggc aac tat gtg gtg caa tat ata att acc aaa gag    3023
Leu Asp Pro Phe Gly Asn Tyr Val Val Gln Tyr Ile Ile Thr Lys Glu
    755             760             765

gct gag aag aac aaa tat gat tat acg cat aaa att gtc cac ctg ttg    3071
Ala Glu Lys Asn Lys Tyr Asp Tyr Thr His Lys Ile Val His Leu Leu
770             775             780             785

aaa cca aga gcc atc gaa ctt tct atc cat aaa ttt gga tca aat gtg    3119
Lys Pro Arg Ala Ile Glu Leu Ser Ile His Lys Phe Gly Ser Asn Val
            790             795             800

att gaa aaa atc ttg aag aca gct att gtt tcg gag cca atg att ctg    3167
Ile Glu Lys Ile Leu Lys Thr Ala Ile Val Ser Glu Pro Met Ile Leu
            805             810             815

gaa att tta aat aat ggt ggc gag acg ggt att caa tca ttg ttg aat    3215
Glu Ile Leu Asn Asn Gly Gly Glu Thr Gly Ile Gln Ser Leu Leu Asn
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                820                      825                      830
     gat agc tac gga aat tac gtt tta cag aca gca tta gac att tct cat   3263
     Asp Ser Tyr Gly Asn Tyr Val Leu Gln Thr Ala Leu Asp Ile Ser His
         835                      840                      845

     aag caa aat gac tat ctc tat aaa aga cta tca gag att gtg gcg cct   3311
     Lys Gln Asn Asp Tyr Leu Tyr Lys Arg Leu Ser Glu Ile Val Ala Pro
     850                      855                      860                      865

     tta ctg gtg ggc ccc ata aga aat aca cct cat ggt aaa aga atc atc   3359
     Leu Leu Val Gly Pro Ile Arg Asn Thr Pro His Gly Lys Arg Ile Ile
                         870                      875                      880

     gga atg tta cat tta gat tca tagttgatac atatatcctc agtttagctt       3410
     Gly Met Leu His Leu Asp Ser
                     885

     tttttacgtt agcctcatat aatatctttt gtacaatact aaaatacatc attttttttt 3470
     tcgttgagga tcaaatgaat atccaaagca aaaaaaatag gaattttcac tttatggtat 3530
     actggtaaat agtgttgaag aaataagaga aggagatcgc cctagaaaac agaatgttct 3590
     tatttaaata agtaaactca aaagaaaaaa aaaggaagg aagtttttga gaacttttat 3650
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     Leu Asp Asp Pro Glu Glu Asn Ala Thr Ser Asn Ala Phe Ala Asn Lys
             35                  40                  45
     Val Ser Gln Asp Ser Gln Phe Ala Asn Gly Pro Pro Ser Gln Met Phe
         50                  55                  60
     Pro His Pro Gln Met Met Gly Gly Met Gly Phe Met Pro Tyr Ser Gln
     65                  70                  75                  80
     Met Met Gln Val Pro His Asn Pro Cys Pro Phe Phe Pro Pro Pro Asp
                 85                  90                  95
     Phe Asn Asp Pro Thr Ala Pro Leu Ser Ser Ser Pro Leu Asn Ala Gly
                 100                 105                 110
     Gly Pro Pro Met Leu Phe Lys Asn Asp Ser Leu Pro Phe Gln Met Leu
             115                 120                 125
     Ser Ser Gly Ala Ala Val Ala Thr Gln Gly Gly Gln Asn Leu Asn Pro
         130                 135                 140
     Leu Ile Asn Asp Asn Ser Met Lys Val Leu Pro Ile Ala Ser Ala Asp
     145                 150                 155                 160
     Pro Leu Trp Thr His Ser Asn Val Pro Gly Ser Ala Ser Val Ala Ile
                     165                 170                 175
     Glu Glu Thr Thr Ala Thr Leu Gln Glu Ser Leu Pro Ser Lys Gly Arg
                 180                 185                 190
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Leu Ser Pro Thr Asp Leu Ile Asn Ala Ala Asn Asn Val Thr Leu Ser
        210             215             220
Lys Asp Phe Gln Ser Asp Met Gln Asn Phe Ser Lys Ala Lys Lys Pro
225             230             235             240
Ser Val Gly Ala Asn Asn Thr Ala Lys Thr Arg Thr Gln Ser Ile Ser
        245             250             255
Phe Asp Asn Thr Pro Ser Ser Thr Ser Phe Ile Pro Pro Thr Asn Ser
        260             265             270
Val Ser Glu Lys Leu Ser Asp Phe Lys Ile Glu Thr Ser Lys Glu Asp
        275             280             285
Leu Ile Asn Lys Thr Ala Pro Ala Lys Lys Glu Ser Pro Thr Thr Tyr
        290             295             300
Gly Ala Ala Tyr Pro Tyr Gly Gly Pro Leu Leu Gln Pro Asn Pro Ile
305             310             315             320
Met Pro Gly His Pro His Asn Ile Ser Ser Pro Ile Tyr Gly Ile Arg
        325             330             335
Ser Pro Phe Pro Asn Ser Tyr Glu Met Gly Ala Gln Phe Gln Pro Phe
        340             345             350
Ser Pro Ile Leu Asn Pro Thr Ser His Ser Leu Asn Ala Asn Ser Pro
        355             360             365
Ile Pro Leu Thr Gln Ser Pro Ile His Leu Ala Pro Val Leu Asn Pro
        370             375             380
Ser Ser Asn Ser Val Ala Phe Ser Asp Met Lys Asn Asp Gly Gly Lys
385             390             395             400
Pro Thr Thr Asp Asn Asp Lys Ala Gly Pro Asn Val Arg Met Asp Leu
        405             410             415
Ile Asn Pro Asn Leu Gly Pro Ser Met Gln Pro Phe His Ile Leu Pro
        420             425             430
Pro Gln Gln Asn Thr Pro Pro Pro Trp Leu Tyr Ser Thr Pro Pro
        435             440             445
Pro Phe Asn Ala Met Val Pro Pro His Leu Leu Ala Gln Asn His Met
        450             455             460
Pro Leu Met Asn Ser Ala Asn Asn Lys His His Gly Arg Asn Asn Asn
465             470             475             480
Ser Met Ser Ser His Asn Asp Asn Asp Asn Ile Gly Asn Ser Asn Tyr
        485             490             495
Asn Asn Lys Asp Thr Gly Arg Ser Asn Val Gly Lys Met Lys Asn Met
        500             505             510
Lys Asn Ser Tyr His Gly Tyr Tyr Asn Asn Asn Asn Asn Asn Asn Asn
        515             520             525
Asn Asn Asn Asn Asn Asn Ser Asn Ala Thr Asn Ser Asn Ser Ala
        530             535             540
Glu Lys Gln Arg Lys Ile Glu Glu Ser Ser Arg Phe Ala Asp Ala Val
545             550             555             560
Leu Asp Gln Tyr Ile Gly Ser Ile His Ser Leu Cys Lys Asp Gln His
        565             570             575
Gly Cys Arg Phe Leu Gln Lys Gln Leu Asp Ile Leu Gly Ser Lys Ala
        580             585             590
Ala Asp Arg Ile Phe Glu Glu Thr Lys Asp Tyr Thr Val Glu Leu Met
        595             600             605
Thr Asp Ser Phe Gly Asn Tyr Leu Ile Gln Lys Leu Leu Glu Glu Val
        610             615             620
Thr Thr Glu Gln Arg Ile Val Leu Thr Lys Ile Ser Ser Pro His Phe
625             630             635             640
Val Glu Ile Ser Leu Asn Pro His Gly Thr Arg Ala Leu Gln Lys Leu
        645             650             655
Ile Glu Cys Ile Lys Thr Asp Glu Glu Ala Gln Ile Val Val Asp Ser
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                660                         665                         670
Leu Arg Pro Tyr Thr Val Gln Leu Ser Lys Asp Leu Asn Gly Asn His
        675                         680                     685
Val Ile Gln Lys Cys Leu Gln Arg Leu Lys Pro Glu Asn Phe Gln Phe
    690                         695                     700
Ile Phe Asp Ala Ile Ser Asp Ser Cys Ile Asp Ile Ala Thr His Arg
705                     710                         715                     720
His Gly Cys Cys Val Leu Gln Arg Cys Leu Asp His Gly Thr Thr Glu
                725                         730                     735
Gln Cys Asp Asn Leu Cys Asp Lys Leu Leu Ala Leu Val Asp Lys Leu
            740                         745                     750
Thr Leu Asp Pro Phe Gly Asn Tyr Val Val Gln Tyr Ile Ile Thr Lys
        755                         760                     765
Glu Ala Glu Lys Asn Lys Tyr Asp Tyr Thr His Lys Ile Val His Leu
    770                         775                     780
Leu Lys Pro Arg Ala Ile Glu Leu Ser Ile His Lys Phe Gly Ser Asn
785                     790                         795                     800
Val Ile Glu Lys Ile Leu Lys Thr Ala Ile Val Ser Glu Pro Met Ile
                805                         810                     815
Leu Glu Ile Leu Asn Asn Gly Gly Glu Thr Gly Ile Gln Ser Leu Leu
            820                         825                     830
Asn Asp Ser Tyr Gly Asn Tyr Val Leu Gln Thr Ala Leu Asp Ile Ser
        835                         840                     845
His Lys Gln Asn Asp Tyr Leu Tyr Lys Arg Leu Ser Glu Ile Val Ala
    850                         855                     860
Pro Leu Leu Val Gly Pro Ile Arg Asn Thr Pro His Gly Lys Arg Ile
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Ile Gly Met Leu His Leu Asp Ser
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Ser Val Ala Cys Val Leu Lys Arg Lys Ala Val Leu Trp Gln Asp Ser
            5                   10                      15


ttc agc ccc cac ctg aaa cat cac cct caa gaa cca gct aat ccc aac   155
Phe Ser Pro His Leu Lys His His Pro Gln Glu Pro Ala Asn Pro Asn
        20                      25                      30


atg cct gtt gtt ttg aca tct gga aca ggg tcg caa gcg cag cca caa   203
Met Pro Val Val Leu Thr Ser Gly Thr Gly Ser Gln Ala Gln Pro Gln
    35                      40                      45


cca gct gca aat cag gct ctt gca gct ggg act cac tcc agc cct gtc   251
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Pro Ala Ala Asn Gln Ala Leu Ala Ala Gly Thr His Ser Ser Pro Val
 50              55              60                  65


cca gga tct ata gga gtt gca ggc cgt tcc cag gac gac gct atg gtg    299
Pro Gly Ser Ile Gly Val Ala Gly Arg Ser Gln Asp Asp Ala Met Val
                70              75                  80


gac tac ttc ttt cag agg cag cat ggt gag cag ctt ggg gga gga gga    347
Asp Tyr Phe Phe Gln Arg Gln His Gly Glu Gln Leu Gly Gly Gly Gly
                85              90                  95


agt gga gga ggc ggc tat aat aat agc aaa cat cga tgg cct act ggg    395
Ser Gly Gly Gly Gly Tyr Asn Asn Ser Lys His Arg Trp Pro Thr Gly
            100             105             110


gat aac att cat gca gaa cat cag gtg cgt tcc atg gat gaa ctg aat    443
Asp Asn Ile His Ala Glu His Gln Val Arg Ser Met Asp Glu Leu Asn
        115             120             125


cat gat ttt caa gca ctt gct ctg gag gga aga gcg atg gga gag cag    491
His Asp Phe Gln Ala Leu Ala Leu Glu Gly Arg Ala Met Gly Glu Gln
130             135             140                 145


ctc ttg cca ggt aaa aag ttt tgg gaa aca gat gaa tcc agc aaa gat    539
Leu Leu Pro Gly Lys Lys Phe Trp Glu Thr Asp Glu Ser Ser Lys Asp
                150             155             160


gga cca aaa gga ata ttc ctg ggt gat caa tgg cga gac agt gcc tgg    587
Gly Pro Lys Gly Ile Phe Leu Gly Asp Gln Trp Arg Asp Ser Ala Trp
                165             170             175


gga aca tca gat cat tca gtt tcc cag cca atc atg gtg cag aga aga    635
Gly Thr Ser Asp His Ser Val Ser Gln Pro Ile Met Val Gln Arg Arg
            180             185             190


cct ggt cag agt ttc cat gtg aac agt gag gtc aat tct gta ctg tcc    683
Pro Gly Gln Ser Phe His Val Asn Ser Glu Val Asn Ser Val Leu Ser
        195             200             205


cca cga tcg gag agt ggg gga cta ggc gtt agc atg gtg gag tat gtg    731
Pro Arg Ser Glu Ser Gly Gly Leu Gly Val Ser Met Val Glu Tyr Val
210             215             220                 225


ttg agc tca tcc ccg ggc gat tcc tgt cta aga aaa gga gga ttt ggc    779
Leu Ser Ser Ser Pro Gly Asp Ser Cys Leu Arg Lys Gly Gly Phe Gly
                230             235             240


cca agg gat gca gac agt gat gaa aac gac aaa ggt gaa aag aag aac    827
Pro Arg Asp Ala Asp Ser Asp Glu Asn Asp Lys Gly Glu Lys Lys Asn
                245             250             255


aag ggt acg ttt gat gga gat aag cta gga gat ttg aag gag gag ggt    875
Lys Gly Thr Phe Asp Gly Asp Lys Leu Gly Asp Leu Lys Glu Glu Gly
                260             265             270


gat gtg atg gac aag acc aat ggt tta cca gtg cag aat ggg att gat    923
Asp Val Met Asp Lys Thr Asn Gly Leu Pro Val Gln Asn Gly Ile Asp
        275             280             285
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gca gac gtc aaa gat ttt agc cgt acc cct ggt aat tgc cag aac tct    971
Ala Asp Val Lys Asp Phe Ser Arg Thr Pro Gly Asn Cys Gln Asn Ser
290             295             300             305

gct aat gaa gtg gat ctt ctg ggt cca aac cag aat ggt tct gag ggc   1019
Ala Asn Glu Val Asp Leu Leu Gly Pro Asn Gln Asn Gly Ser Glu Gly
                310             315             320

tta gcc cag ctg acc agc acc aat ggt gcc aag cct gtg gag gat ttc   1067
Leu Ala Gln Leu Thr Ser Thr Asn Gly Ala Lys Pro Val Glu Asp Phe
            325             330             335

tcc aac atg gag tcc cag agt gtc ccc ttg gac ccc atg gaa cat gtg   1115
Ser Asn Met Glu Ser Gln Ser Val Pro Leu Asp Pro Met Glu His Val
        340             345             350

ggc atg gag cct ctt cag ttt gat tat tca ggc acg cag gta cct gtg   1163
Gly Met Glu Pro Leu Gln Phe Asp Tyr Ser Gly Thr Gln Val Pro Val
        355             360             365

gac tca gca gca gca act gtg gga ctt ttt gac tac aat tct caa caa   1211
Asp Ser Ala Ala Ala Thr Val Gly Leu Phe Asp Tyr Asn Ser Gln Gln
370             375             380             385

cag ctg ttc caa aga cct aat gcg ctt gct gtc cag cag ttg aca gct   1259
Gln Leu Phe Gln Arg Pro Asn Ala Leu Ala Val Gln Gln Leu Thr Ala
            390             395             400

gct cag cag cag cag tat gca ctg gca gct gct cat cag ccg cac atc   1307
Ala Gln Gln Gln Gln Tyr Ala Leu Ala Ala Ala His Gln Pro His Ile
            405             410             415

ggt tta gct ccc gct gcg ttt gtc ccc aat cca tac atc atc agc gct   1355
Gly Leu Ala Pro Ala Ala Phe Val Pro Asn Pro Tyr Ile Ile Ser Ala
            420             425             430

gct ccc cca ggg acg gac ccc tac aca gct gga ttg gct gca gca gcg   1403
Ala Pro Pro Gly Thr Asp Pro Tyr Thr Ala Gly Leu Ala Ala Ala Ala
            435             440             445

aca cta ggc cca gct gtg gtc cct cac cag tat tat gga gtt act ccc   1451
Thr Leu Gly Pro Ala Val Val Pro His Gln Tyr Tyr Gly Val Thr Pro
450             455             460             465

tgg gga gtc tac cct gcc agt ctt ttc cag cag caa gct gcc gct gcc   1499
Trp Gly Val Tyr Pro Ala Ser Leu Phe Gln Gln Gln Ala Ala Ala Ala
                470             475             480

gct gca gca act aat tca gct aat caa cag acc acc cca cag gct cag   1547
Ala Ala Ala Thr Asn Ser Ala Asn Gln Gln Thr Thr Pro Gln Ala Gln
                485             490             495

caa gga cag cag cag gtt ctc cgt gga gga gcc agc caa cgt cct ttg   1595
Gln Gly Gln Gln Gln Val Leu Arg Gly Gly Ala Ser Gln Arg Pro Leu
            500             505             510

acc cca aac cag aac cag cag gga cag caa acg gat ccc ctt gtg gca   1643
Thr Pro Asn Gln Asn Gln Gln Gly Gln Gln Thr Asp Pro Leu Val Ala
        515             520             525
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gct gca gca gtg aat tct gcc ctt gca ttt gga caa ggt ctg gca gca    1691
Ala Ala Ala Val Asn Ser Ala Leu Ala Phe Gly Gln Gly Leu Ala Ala
530             535             540                 545

ggc atg cca ggt tat ccg gtg ttg gct cct gct gct tac tat gac caa    1739
Gly Met Pro Gly Tyr Pro Val Leu Ala Pro Ala Ala Tyr Tyr Asp Gln
                550             555                 560

act ggt gcc ctt gta gtg aat gca ggc gcg aga aat ggt ctt gga gct    1787
Thr Gly Ala Leu Val Val Asn Ala Gly Ala Arg Asn Gly Leu Gly Ala
            565             570             575

cct gtt cga ctt gta gct cct gcc cca gtc atc att agt tcc tca gct    1835
Pro Val Arg Leu Val Ala Pro Ala Pro Val Ile Ile Ser Ser Ser Ala
            580             585             590

gca caa gca gct gtt gca gca gcc gca gct tca gca aat gga gca gct    1883
Ala Gln Ala Ala Val Ala Ala Ala Ala Ala Ser Ala Asn Gly Ala Ala
    595             600             605

ggt ggt ctt gct gga aca aca aat gga cca ttt cgc cct tta gga aca    1931
Gly Gly Leu Ala Gly Thr Thr Asn Gly Pro Phe Arg Pro Leu Gly Thr
610             615             620             625

cag cag cct cag ccc cag ccc cag cag cag ccc aat aac aac ctg gca    1979
Gln Gln Pro Gln Pro Gln Pro Gln Gln Gln Pro Asn Asn Asn Leu Ala
            630             635             640

tcc agt tct ttc tac ggc aac aac tct ctg aac agc aat tca cag agc    2027
Ser Ser Ser Phe Tyr Gly Asn Asn Ser Leu Asn Ser Asn Ser Gln Ser
            645             650             655

agc tcc ctc ttc tcc cag ggc tct gcc cag cct gcc aac aca tcc ttg    2075
Ser Ser Leu Phe Ser Gln Gly Ser Ala Gln Pro Ala Asn Thr Ser Leu
            660             665             670

gga ttc gga agt agc agt tct ctc ggc gcc acc ctg gga tcc gcc ctt    2123
Gly Phe Gly Ser Ser Ser Ser Leu Gly Ala Thr Leu Gly Ser Ala Leu
    675             680             685

gga ggg ttt gga aca gca gtt gca aac tcc aac act ggc agt ggc tcc    2171
Gly Gly Phe Gly Thr Ala Val Ala Asn Ser Asn Thr Gly Ser Gly Ser
690             695             700             705

cgc cgt gac tcc ctg act ggc agc agt gac ctt tat aag agg aca tcg    2219
Arg Arg Asp Ser Leu Thr Gly Ser Ser Asp Leu Tyr Lys Arg Thr Ser
            710             715             720

agc agc ttg acc ccc att gga cac agt ttt tat aac ggc ctt agc ttt    2267
Ser Ser Leu Thr Pro Ile Gly His Ser Phe Tyr Asn Gly Leu Ser Phe
            725             730             735

tcc tcc tct cct gga ccc gtg ggc atg cct ctc cct agt cag gga cca    2315
Ser Ser Ser Pro Gly Pro Val Gly Met Pro Leu Pro Ser Gln Gly Pro
            740             745             750

gga cat tca cag aca cca cct cct tcc ctc tct tca cat gga tcc tct    2363
Gly His Ser Gln Thr Pro Pro Pro Ser Leu Ser Ser His Gly Ser Ser
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            755                    760                      765

tca agc tta aac ctg gga gga ctc acg aat ggc agt gga aga tac atc   2411
Ser Ser Leu Asn Leu Gly Gly Leu Thr Asn Gly Ser Gly Arg Tyr Ile
770                 775                 780                 785

tct gct gct cca ggc gct gaa gcc aag tac cgc agt gca agc agc gcc   2459
Ser Ala Ala Pro Gly Ala Glu Ala Lys Tyr Arg Ser Ala Ser Ser Ala
                790                 795                 800

tcc agc ctc ttc agc ccg agc agc act ctt ttc tct tcc tct cgt ttg   2507
Ser Ser Leu Phe Ser Pro Ser Ser Thr Leu Phe Ser Ser Ser Arg Leu
                805                 810                 815

cga tat gga atg tct gat gtc atg cct tct ggc agg agc agg ctt ttg   2555
Arg Tyr Gly Met Ser Asp Val Met Pro Ser Gly Arg Ser Arg Leu Leu
                820                 825                 830

gaa gat ttt cga aac aac cgg tac ccc aat tta caa ctg cgg gag att   2603
Glu Asp Phe Arg Asn Asn Arg Tyr Pro Asn Leu Gln Leu Arg Glu Ile
    835                 840                 845

gct gga cat ata atg gaa ttt tcc caa gac cag cat ggg tcc aga ttc   2651
Ala Gly His Ile Met Glu Phe Ser Gln Asp Gln His Gly Ser Arg Phe
850                 855                 860                 865

att cag ctg aaa ctg gag cgt gcc aca cca gct gag cgc cag ctt gtc   2699
Ile Gln Leu Lys Leu Glu Arg Ala Thr Pro Ala Glu Arg Gln Leu Val
                870                 875                 880

ttc aat gaa atc ctc cag gct gcc tac caa ctc atg gtg gat gtg ttt   2747
Phe Asn Glu Ile Leu Gln Ala Ala Tyr Gln Leu Met Val Asp Val Phe
                885                 890                 895

ggt aat tac gtc att cag aag ttc ttt gaa ttt ggc agt ctt gaa cag   2795
Gly Asn Tyr Val Ile Gln Lys Phe Phe Glu Phe Gly Ser Leu Glu Gln
                900                 905                 910

aag ctg gct ttg gca gaa cgg att cga ggc cac gtc ctg tca ttg gca   2843
Lys Leu Ala Leu Ala Glu Arg Ile Arg Gly His Val Leu Ser Leu Ala
    915                 920                 925

cta cag atg tat ggc tgc cgt gtt atc cag aaa gct ctt gag ttt att   2891
Leu Gln Met Tyr Gly Cys Arg Val Ile Gln Lys Ala Leu Glu Phe Ile
930                 935                 940                 945

cct tca gac cag cag aat gag atg gtt cgg gaa cta gat ggc cat gtc   2939
Pro Ser Asp Gln Gln Asn Glu Met Val Arg Glu Leu Asp Gly His Val
                950                 955                 960

ttg aag tgt gtg aaa gat cag aat ggc aat cac gtg gtt cag aaa tgc   2987
Leu Lys Cys Val Lys Asp Gln Asn Gly Asn His Val Val Gln Lys Cys
                965                 970                 975

att gaa tgt gta cag ccc cag tct ttg caa ttt atc atc gat gcg ttt   3035
Ile Glu Cys Val Gln Pro Gln Ser Leu Gln Phe Ile Ile Asp Ala Phe
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aag gga cag gta ttt gcc tta tcc aca cat cct tat ggc tgc cga gtg   3083
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Lys Gly Gln Val Phe Ala Leu Ser Thr His Pro Tyr Gly Cys Arg Val
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att cag aga atc ctg gag cac tgt ctc cct gac cag aca ctc cct att   3131
Ile Gln Arg Ile Leu Glu His Cys Leu Pro Asp Gln Thr Leu Pro Ile
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tta gag gag ctt cac cag cac aca gag cag ctt gta cag gat caa tat   3179
Leu Glu Glu Leu His Gln His Thr Glu Gln Leu Val Gln Asp Gln Tyr
                1030   1035   1040

gga aat tat gta atc caa cat gta ctg gag cac ggt cgt cct gag gat   3227
Gly Asn Tyr Val Ile Gln His Val Leu Glu His Gly Arg Pro Glu Asp
                1045   1050   1055

aaa agc aaa att gta gca gaa atc cga ggc aat gta ctt gta ttg agt   3275
Lys Ser Lys Ile Val Ala Glu Ile Arg Gly Asn Val Leu Val Leu Ser
                1060   1065   1070

cag cac aaa ttt gca agc aat gtt gtg gag aag tgt gtt act cac gcc   3323
Gln His Lys Phe Ala Ser Asn Val Val Glu Lys Cys Val Thr His Ala
        1075   1080   1085

tca cgt acg gag cgc gct gtg ctc atc gat gag gtg tgc acc atg aac   3371
Ser Arg Thr Glu Arg Ala Val Leu Ile Asp Glu Val Cys Thr Met Asn
1090   1095   1100   1105

gac ggt ccc cac agt gcc tta tac acc atg atg aag gac cag tat gcc   3419
Asp Gly Pro His Ser Ala Leu Tyr Thr Met Met Lys Asp Gln Tyr Ala
                1110   1115   1120

aac tac gtg gtc cag aag atg att gac gtg gcg gag cca ggc cag cgg   3467
Asn Tyr Val Val Gln Lys Met Ile Asp Val Ala Glu Pro Gly Gln Arg
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aag atc gtc atg cat aag atc cgg ccc cac atc gca act ctt cgt aag   3515
Lys Ile Val Met His Lys Ile Arg Pro His Ile Ala Thr Leu Arg Lys
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tac acc tat ggc aag cac att ctg gcc aag ctg gag aag tac tac atg   3563
Tyr Thr Tyr Gly Lys His Ile Leu Ala Lys Leu Glu Lys Tyr Tyr Met
        1155   1160   1165

aag aac ggt gtt gac tta ggg ccc atc tgt ggc ccc cct aat ggt atc   3611
Lys Asn Gly Val Asp Leu Gly Pro Ile Cys Gly Pro Pro Asn Gly Ile
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Asn Met Pro Val Val Leu Thr Ser Gly Thr Gly Ser Gln Ala Gln Pro
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Gln Pro Ala Ala Asn Gln Ala Leu Ala Ala Gly Thr His Ser Ser Pro
    50                  55                  60
Val Pro Gly Ser Ile Gly Val Ala Gly Arg Ser Gln Asp Asp Ala Met
65                  70                  75                  80
Val Asp Tyr Phe Phe Gln Arg Gln His Gly Glu Gln Leu Gly Gly Gly
                85                  90                  95
Gly Ser Gly Gly Gly Gly Tyr Asn Asn Ser Lys His Arg Trp Pro Thr
                100                 105                 110
Gly Asp Asn Ile His Ala Glu His Gln Val Arg Ser Met Asp Glu Leu
            115                 120                 125
Asn His Asp Phe Gln Ala Leu Ala Leu Glu Gly Arg Ala Met Gly Glu
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Gln Leu Leu Pro Gly Lys Lys Phe Trp Glu Thr Asp Glu Ser Ser Lys
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Asp Gly Pro Lys Gly Ile Phe Leu Gly Asp Gln Trp Arg Asp Ser Ala
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Trp Gly Thr Ser Asp His Ser Val Ser Gln Pro Ile Met Val Gln Arg
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Arg Pro Gly Gln Ser Phe His Val Asn Ser Glu Val Asn Ser Val Leu
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Ser Pro Arg Ser Glu Ser Gly Gly Leu Gly Val Ser Met Val Glu Tyr
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Gly Pro Arg Asp Ala Asp Ser Asp Glu Asn Asp Lys Gly Glu Lys Lys
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Asp Ala Asp Val Lys Asp Phe Ser Arg Thr Pro Gly Asn Cys Gln Asn
        290   295   300
Ser Ala Asn Glu Val Asp Leu Leu Gly Pro Asn Gln Asn Gly Ser Glu
305   310   315   320
Gly Leu Ala Gln Leu Thr Ser Thr Asn Gly Ala Lys Pro Val Glu Asp
                325   330   335
Phe Ser Asn Met Glu Ser Gln Ser Val Pro Leu Asp Pro Met Glu His
                340   345   350
Val Gly Met Glu Pro Leu Gln Phe Asp Tyr Ser Gly Thr Gln Val Pro
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Val Asp Ser Ala Ala Ala Thr Val Gly Leu Phe Asp Tyr Asn Ser Gln
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Gln Gln Leu Phe Gln Arg Pro Asn Ala Leu Ala Val Gln Gln Leu Thr
385   390   395   400
Ala Ala Gln Gln Gln Gln Tyr Ala Leu Ala Ala Ala His Gln Pro His
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Ile Gly Leu Ala Pro Ala Ala Phe Val Pro Asn Pro Tyr Ile Ile Ser
                420   425   430
Ala Ala Pro Pro Gly Thr Asp Pro Tyr Thr Ala Gly Leu Ala Ala Ala
        435   440   445
Ala Thr Leu Gly Pro Ala Val Val Pro His Gln Tyr Tyr Gly Val Thr
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Pro Trp Gly Val Tyr Pro Ala Ser Leu Phe Gln Gln Gln Ala Ala Ala
465   470   475   480
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Ala Pro Val Arg Leu Val Ala Pro Ala Pro Val Ile Ile Ser Ser Ser
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Ala Ala Gln Ala Ala Val Ala Ala Ala Ala Ser Ala Asn Gly Ala
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Thr Gln Gln Pro Gln Pro Gln Pro Gln Gln Gln Pro Asn Asn Asn Leu
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Ala Ser Ser Ser Phe Tyr Gly Asn Asn Ser Leu Asn Ser Asn Ser Gln
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Ser Ser Ser Leu Phe Ser Gln Gly Ser Ala Gln Pro Ala Asn Thr Ser
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Leu Gly Phe Gly Ser Ser Ser Ser Leu Gly Ala Thr Leu Gly Ser Ala
        675   680   685
Leu Gly Gly Phe Gly Thr Ala Val Ala Asn Ser Asn Thr Gly Ser Gly
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Ser Arg Arg Asp Ser Leu Thr Gly Ser Ser Asp Leu Tyr Lys Arg Thr
705   710   715   720
Ser Ser Ser Leu Thr Pro Ile Gly His Ser Phe Tyr Asn Gly Leu Ser

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Leu Glu Asp Phe Arg Asn Asn Arg Tyr Pro Asn Leu Gln Leu Arg Glu
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Ile Ala Gly His Ile Met Glu Phe Ser Gln Asp Gln His Gly Ser Arg
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Phe Gly Asn Tyr Val Ile Gln Lys Phe Phe Glu Phe Gly Ser Leu Glu
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Gln Lys Leu Ala Leu Ala Glu Arg Ile Arg Gly His Val Leu Ser Leu
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Ala Leu Gln Met Tyr Gly Cys Arg Val Ile Gln Lys Ala Leu Glu Phe
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Ile Pro Ser Asp Gln Gln Asn Glu Met Val Arg Glu Leu Asp Gly His
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Val Leu Lys Cys Val Lys Asp Gln Asn Gly Asn His Val Val Gln Lys
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Cys Ile Glu Cys Val Gln Pro Gln Ser Leu Gln Phe Ile Ile Asp Ala
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Phe Lys Gly Gln Val Phe Ala Leu Ser Thr His Pro Tyr Gly Cys Arg
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Val Ile Gln Arg Ile Leu Glu His Cys Leu Pro Asp Gln Thr Leu Pro
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Ile Leu Glu Glu Leu His Gln His Thr Glu Gln Leu Val Gln Asp Gln
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Tyr Gly Asn Tyr Val Ile Gln His Val Leu Glu His Gly Arg Pro Glu
            1045                1050                1055
Asp Lys Ser Lys Ile Val Ala Glu Ile Arg Gly Asn Val Leu Val Leu
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Ser Gln His Lys Phe Ala Ser Asn Val Val Glu Lys Cys Val Thr His
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Ala Ser Arg Thr Glu Arg Ala Val Leu Ile Asp Glu Val Cys Thr Met
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Asn Asp Gly Pro His Ser Ala Leu Tyr Thr Met Met Lys Asp Gln Tyr
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gcaaagcaga caactcagtg ataaaaccaa ctatgacatt gttgttcggg caaagcag 418
atg tgg gag att tta aga aga aaa gac tgt gac aaa gaa aaa aga gta 466
aag tta atg agt gat ttg cag aag ttg att caa ggg aaa att aaa act 514
Met Trp Glu Ile Leu Arg Arg Lys Asp Cys Asp Lys Glu Lys Arg Val
1   5   10   15

att gca ttt gca cac gat tca act cgt gtg atc cag tgt tac att cag 562
Lys Leu Met Ser Asp Leu Gln Lys Leu Ile Gln Gly Lys Ile Lys Thr
            20   25   30

tat ggt aat gaa gaa cag aga aaa cag gct ttt gaa gaa ttg cga gat 610
Ile Ala Phe Ala His Asp Ser Thr Arg Val Ile Gln Cys Tyr Ile Gln
            35   40   45

gat ttg gtt gag tta agt aaa gcc aaa tat tcg aga aat att gtt aag 658
Tyr Gly Asn Glu Glu Gln Arg Lys Gln Ala Phe Glu Glu Leu Arg Asp
        50   55   60

aaa ttt ctc atg tat gga agt aaa cca cag att gca gag ata atc aga 706
Asp Leu Val Glu Leu Ser Lys Ala Lys Tyr Ser Arg Asn Ile Val Lys
65   70   75   80

agt ttt aaa ggc cac gtg agg aag atg ctg cgg cat gcg gaa gca tca 754
Lys Phe Leu Met Tyr Gly Ser Lys Pro Gln Ile Ala Glu Ile Ile Arg
                85   90   95

gcc atc gtg gag tac gca tac aat gac aaa gcc att ttg gag cag agg 802
Ser Phe Lys Gly His Val Arg Lys Met Leu Arg His Ala Glu Ala Ser
                100   105   110

aac atg ctg acg gaa gag ctc tat ggg aac aca ttt cag ctt tac aag 850
Ala Ile Val Glu Tyr Ala Tyr Asn Asp Lys Ala Ile Leu Glu Gln Arg
            115   120   125

tca gca gat cac cga act ctg gac aaa gtg tta gag gta cag cca gaa 898
Asn Met Leu Thr Glu Glu Leu Tyr Gly Asn Thr Phe Gln Leu Tyr Lys
        130   135   140

aaa tta gaa ctt att atg gat gaa atg aaa cag att cta act cca atg 946
Ser Ala Asp His Arg Thr Leu Asp Lys Val Leu Glu Val Gln Pro Glu
145   150   155   160

```
gcc caa aag gaa gct gtg att aag cac tca ttg gtg cat aaa gta ttc    994
Lys Leu Glu Leu Ile Met Asp Glu Met Lys Gln Ile Leu Thr Pro Met
            165             170             175

ttg gac ttt ttt acc tat gca ccc ccc aaa ctc aga tca gaa atg att   1042
Ala Gln Lys Glu Ala Val Ile Lys His Ser Leu Val His Lys Val Phe
            180             185             190

gaa gcc atc cgc gaa gcg gtg gtc tac ctg gca cac aca cac gat ggc   1090
Leu Asp Phe Phe Thr Tyr Ala Pro Pro Lys Leu Arg Ser Glu Met Ile
            195             200             205

gcc aga gtg gcc atg cac tgc ctg tgg cat ggc acg ccc aag gac agg   1138
Glu Ala Ile Arg Glu Ala Val Val Tyr Leu Ala His Thr His Asp Gly
        210             215             220

aaa gtg att gtg aaa aca atg aag act tat gtt gaa aag gtg gct aat   1186
Ala Arg Val Ala Met His Cys Leu Trp His Gly Thr Pro Lys Asp Arg
225             230             235             240

ggc caa tac tcc cat ttg gtt tta ctg gcg gca ttt gat tgt att gat   1234
Lys Val Ile Val Lys Thr Met Lys Thr Tyr Val Glu Lys Val Ala Asn
            245             250             255

gat act aag ctt gtg aag cag ata atc ata tca gaa att atc agt tca   1282
Gly Gln Tyr Ser His Leu Val Leu Leu Ala Ala Phe Asp Cys Ile Asp
            260             265             270

ttg cct agc ata gta aat gac aaa tat gga agg aag gtc cta ttg tac   1330
Asp Thr Lys Leu Val Lys Gln Ile Ile Ile Ser Glu Ile Ile Ser Ser
            275             280             285

tta cta agc ccc aga gat cct gca cat aca gta cga gaa atc att gaa   1378
Leu Pro Ser Ile Val Asn Asp Lys Tyr Gly Arg Lys Val Leu Leu Tyr
        290             295             300

gtt ctg caa aaa gga gat gga aat gca cac agt aag aaa gat aca gag   1426
Leu Leu Ser Pro Arg Asp Pro Ala His Thr Val Arg Glu Ile Ile Glu
305             310             315             320

gtc cgc aga cgg gag ctc cta gaa tcc att tct cca gct ttg tta agc   1474
Val Leu Gln Lys Gly Asp Gly Asn Ala His Ser Lys Lys Asp Thr Glu
            325             330             335

tac ctg caa gaa cac gcc caa gaa gtg gtg cta gat aag tct gcg tgt   1522
Val Arg Arg Arg Glu Leu Leu Glu Ser Ile Ser Pro Ala Leu Leu Ser
            340             345             350

gtg ttg gtg tct gac att ctg gga tct gcc act gga gac gtt cag cct   1570
Tyr Leu Gln Glu His Ala Gln Glu Val Val Leu Asp Lys Ser Ala Cys
            355             360             365

acc atg aat gcc atc gcc agc ttg gca gca aca gga ctg cat cct ggt   1618
Val Leu Val Ser Asp Ile Leu Gly Ser Ala Thr Gly Asp Val Gln Pro
        370             375             380

ggc aag gac gga gag ctt cac att gca gaa cat cct gca gga cat cta   1666
Thr Met Asn Ala Ile Ala Ser Leu Ala Ala Thr Gly Leu His Pro Gly
```

```
385                       390                       395                       400

gtt ctg aag tgg tta ata gag caa gat aaa aag atg aaa gaa aat ggg    1714
Gly Lys Asp Gly Glu Leu His Ile Ala Glu His Pro Ala Gly His Leu
            405                       410                       415

aga gaa ggt tgt ttt gca aaa aca ctt gta gag cat gtt ggt atg aag    1762
Val Leu Lys Trp Leu Ile Glu Gln Asp Lys Lys Met Lys Glu Asn Gly
            420                       425                       430

aac ctg aag tcc tgg gct agt gta aat cga ggt gcc att att ctt tct    1810
Arg Glu Gly Cys Phe Ala Lys Thr Leu Val Glu His Val Gly Met Lys
            435                       440                       445

agc ctc ctc cag agt tgt gac ctg gaa gtt gca aac aaa gtc aaa gct    1858
Asn Leu Lys Ser Trp Ala Ser Val Asn Arg Gly Ala Ile Ile Leu Ser
            450                       455                       460

gca ctg aaa agc ttg att cct aca ctg gaa aaa acc aaa agc acc agc    1906
Ser Leu Leu Gln Ser Cys Asp Leu Glu Val Ala Asn Lys Val Lys Ala
465                       470                       475                       480

aaa gga ata gaa att cta ctt gaa aaa ctg agc aca taggtggaaa         1952
Ala Leu Lys Ser Leu Ile Pro Thr Leu Glu Lys Thr Lys Ser Thr Ser
            485                       490                       495

gagttaagag caagatggaa tgattttttc tgttctctgt tctgtttccc aatgcagaaa  2012
Lys Gly Ile Glu Ile Leu Leu Glu Lys Leu Ser Thr
            500                       505

agaaggggta gggtccacca tactggtaat tggggtactc tgtatatgtg tttcttcttt  2072
gtatacgaat ctattatat aaattgtttt tttaaatggt                         2112
```

<210> 10
<211> 508
<212> PRT
<213> Homo sapiens

<400> 10

```
Met Trp Glu Ile Leu Arg Arg Lys Asp Cys Asp Lys Glu Lys Arg Val
1               5                   10                  15
Lys Leu Met Ser Asp Leu Gln Lys Leu Ile Gln Gly Lys Ile Lys Thr
            20                  25                  30
Ile Ala Phe Ala His Asp Ser Thr Arg Val Ile Gln Cys Tyr Ile Gln
            35                  40                  45
Tyr Gly Asn Glu Glu Gln Arg Lys Gln Ala Phe Glu Glu Leu Arg Asp
        50                  55                  60
Asp Leu Val Glu Leu Ser Lys Ala Lys Tyr Ser Arg Asn Ile Val Lys
65                  70                  75                  80
Lys Phe Leu Met Tyr Gly Ser Lys Pro Gln Ile Ala Glu Ile Ile Arg
                85                  90                  95
Ser Phe Lys Gly His Val Arg Lys Met Leu Arg His Ala Glu Ala Ser
            100                 105                 110
Ala Ile Val Glu Tyr Ala Tyr Asn Asp Lys Ala Ile Leu Glu Gln Arg
            115                 120                 125
Asn Met Leu Thr Glu Glu Leu Tyr Gly Asn Thr Phe Gln Leu Tyr Lys
        130                 135                 140
Ser Ala Asp His Arg Thr Leu Asp Lys Val Leu Glu Val Gln Pro Glu
145                 150                 155                 160
```

```
Lys Leu Glu Leu Ile Met Asp Glu Met Lys Gln Ile Leu Thr Pro Met
                165             170             175
Ala Gln Lys Glu Ala Val Ile Lys His Ser Leu Val His Lys Val Phe
            180             185             190
Leu Asp Phe Phe Thr Tyr Ala Pro Pro Lys Leu Arg Ser Glu Met Ile
        195             200             205
Glu Ala Ile Arg Glu Ala Val Val Tyr Leu Ala His Thr His Asp Gly
    210             215             220
Ala Arg Val Ala Met His Cys Leu Trp His Gly Thr Pro Lys Asp Arg
225             230             235             240
Lys Val Ile Val Lys Thr Met Lys Thr Tyr Val Glu Lys Val Ala Asn
            245             250             255
Gly Gln Tyr Ser His Leu Val Leu Leu Ala Ala Phe Asp Cys Ile Asp
            260             265             270
Asp Thr Lys Leu Val Lys Gln Ile Ile Ile Ser Glu Ile Ile Ser Ser
        275             280             285
Leu Pro Ser Ile Val Asn Asp Lys Tyr Gly Arg Lys Val Leu Leu Tyr
        290             295             300
Leu Leu Ser Pro Arg Asp Pro Ala His Thr Val Arg Glu Ile Ile Glu
305             310             315             320
Val Leu Gln Lys Gly Asp Gly Asn Ala His Ser Lys Lys Asp Thr Glu
            325             330             335
Val Arg Arg Arg Glu Leu Leu Glu Ser Ile Ser Pro Ala Leu Leu Ser
            340             345             350
Tyr Leu Gln Glu His Ala Gln Glu Val Val Leu Asp Lys Ser Ala Cys
        355             360             365
Val Leu Val Ser Asp Ile Leu Gly Ser Ala Thr Gly Asp Val Gln Pro
    370             375             380
Thr Met Asn Ala Ile Ala Ser Leu Ala Ala Thr Gly Leu His Pro Gly
385             390             395             400
Gly Lys Asp Gly Glu Leu His Ile Ala Glu His Pro Ala Gly His Leu
            405             410             415
Val Leu Lys Trp Leu Ile Glu Gln Asp Lys Lys Met Lys Glu Asn Gly
            420             425             430
Arg Glu Gly Cys Phe Ala Lys Thr Leu Val Glu His Val Gly Met Lys
        435             440             445
Asn Leu Lys Ser Trp Ala Ser Val Asn Arg Gly Ala Ile Ile Leu Ser
    450             455             460
Ser Leu Leu Gln Ser Cys Asp Leu Glu Val Ala Asn Lys Val Lys Ala
465             470             475             480
Ala Leu Lys Ser Leu Ile Pro Thr Leu Glu Lys Thr Lys Ser Thr Ser
            485             490             495
Lys Gly Ile Glu Ile Leu Leu Glu Lys Leu Ser Thr
            500             505
```

<210> 11
<211> 2457
<212> DNA
<213> Saccharomyces cerevisiae

<220>
<221> CDS
<222> (645)...(1655)
<223> NCA3

<400> 11
ggatccctct gtgaggccga ttatgcaggc ctagacccgc acgtgaccac ttcgagagca 60
agttgcctgc gagtttctct gcccgaggaa aaagaaatgg aggcaattta cttaatatgg 120

```
tatgagagga tcttttgacg gcaaatagat gcgccatctc cgagaaaaaa tctagacaat 180
aacagcgaca attaacctaa agaggataga agatcgagca aaaaatttt ttaatatggg 240
gtcagtggcg atattatact ataggagtta aagagtaagt tgagtgtaag gtggtagaat 300
tatgattgaa ctccgaaact aagcgccgat tatgggtggc aaagcggaca gcttttgata 360
tataatcgat cgctctcgta gttgatatcc tctctcttgc ttatctttttc ctgtatatag 420
tatatgtgta catacagata cgaatatacc tcagttagtt tgttttaaca ttaaatattc 480
aacagttgcc agtagcaaaa agaatatatc cattcatttc gagcttttttc gtctcattac 540
tgatatccaa ctaacagtct cctcatagac ggtaccttac tttccttttaa tattaaaata 600
ctagtatagt cgcacatact taactcgtct ctctctaaca cata atg aaa att tcc 656
                                                  Met Lys Ile Ser
                                                    1
```

```
gca gct tta ata ttg tct tcc ctt tct tct gtc gca ttt tct gcc cct  704
Ala Ala Leu Ile Leu Ser Ser Leu Ser Ser Val Ala Phe Ser Ala Pro
 5               10                  15                      20
```

```
gca cct gct cca gcg gac agt cat cat gaa gat cat cac aaa gat gaa  752
Ala Pro Ala Pro Ala Asp Ser His His Glu Asp His His Lys Asp Glu
            25                  30                  35
```

```
aaa cca gcg gtt gtc act gtc act caa tac ata gat tcc aat gcc gct  800
Lys Pro Ala Val Val Thr Val Thr Gln Tyr Ile Asp Ser Asn Ala Ala
            40                  45                  50
```

```
act agt act gta gaa tct gct gct act acc act aca ttg tcc tca tct  848
Thr Ser Thr Val Glu Ser Ala Ala Thr Thr Thr Thr Leu Ser Ser Ser
            55                  60                  65
```

```
gag aag gat acc tct gaa cag aag cgt gat ggc gga ttc caa gat ggt  896
Glu Lys Asp Thr Ser Glu Gln Lys Arg Asp Gly Gly Phe Gln Asp Gly
        70                  75                  80
```

```
act gtc aaa tgt tcg gac ttc cct tct gta aac ggt ata gtt tcc ttg  944
Thr Val Lys Cys Ser Asp Phe Pro Ser Val Asn Gly Ile Val Ser Leu
 85                  90                  95                 100
```

```
gac tgg cta gga ttt ggt gga tgg gcc tct gtc atg gac atg gat gcc  992
Asp Trp Leu Gly Phe Gly Gly Trp Ala Ser Val Met Asp Met Asp Ala
                105                 110                 115
```

```
aac act tcg tcc gaa tgt aag gat ggc tac tac tgt tct tat gca tgt  1040
Asn Thr Ser Ser Glu Cys Lys Asp Gly Tyr Tyr Cys Ser Tyr Ala Cys
                120                 125                 130
```

```
gaa cct gga atg tca aag act caa tgg cct tct gac caa cca agc gat  1088
Glu Pro Gly Met Ser Lys Thr Gln Trp Pro Ser Asp Gln Pro Ser Asp
                135                 140                 145
```

```
ggt aaa tct gtt ggt ggt ctt tat tgt aaa aat ggt tac ttg tac cgt  1136
Gly Lys Ser Val Gly Gly Leu Tyr Cys Lys Asn Gly Tyr Leu Tyr Arg
            150                 155                 160
```

```
acc aac act gat acc agc gat tta tgt tct acg gat gaa aca tct gct  1184
Thr Asn Thr Asp Thr Ser Asp Leu Cys Ser Thr Asp Glu Thr Ser Ala
165                 170                 175                 180
```

```
aag gcc att aac aaa aag tct gac tcc att gct cta tgt agg acg gat  1232
Lys Ala Ile Asn Lys Lys Ser Asp Ser Ile Ala Leu Cys Arg Thr Asp
                185                 190                 195
```

```
tac cca gga tct gaa aac atg gtg att ccc aca gtg gtt gat ggt gga    1280
Tyr Pro Gly Ser Glu Asn Met Val Ile Pro Thr Val Val Asp Gly Gly
            200                 205                 210

gat tca caa cca att tca gtc gtt gat gaa gac act tat tat caa tgg    1328
Asp Ser Gln Pro Ile Ser Val Val Asp Glu Asp Thr Tyr Tyr Gln Trp
            215                 220                 225

cag ggt aaa aag act tct gct cag tac tat att aac aac gcc ggt gta    1376
Gln Gly Lys Lys Thr Ser Ala Gln Tyr Tyr Ile Asn Asn Ala Gly Val
            230                 235                 240

tct gca gaa gat ggg tgc att tgg ggt act tct ggt tcg gat gtc ggc    1424
Ser Ala Glu Asp Gly Cys Ile Trp Gly Thr Ser Gly Ser Asp Val Gly
245                 250                 255                 260

aac tgg gct cca cta gtg tta ggt gct ggt tcc act aat gga gaa aca    1472
Asn Trp Ala Pro Leu Val Leu Gly Ala Gly Ser Thr Asn Gly Glu Thr
                265                 270                 275

tac ttg tcg ttg att cca aac ccc aac agt aac caa gct gcc aac ttt    1520
Tyr Leu Ser Leu Ile Pro Asn Pro Asn Ser Asn Gln Ala Ala Asn Phe
            280                 285                 290

aac gtt aaa ata gtt gca tcc gat ggc gct aac gtt cag ggc agc tgt    1568
Asn Val Lys Ile Val Ala Ser Asp Gly Ala Asn Val Gln Gly Ser Cys
            295                 300                 305

gcg tat gaa gat ggc tct ttc acc gga gat ggt tcc gat ggt tgc aca    1616
Ala Tyr Glu Asp Gly Ser Phe Thr Gly Asp Gly Ser Asp Gly Cys Thr
            310                 315                 320

gtt tct gtt tta tct gga tct gct gaa ttt gtt ttc tat taagtcactc    1665
Val Ser Val Leu Ser Gly Ser Ala Glu Phe Val Phe Tyr
325                 330                 335

ttcttttcgg taaaagaatg tcttgtattt tgataccctc aattcccctt attattcttt 1725
ttcttccgct ctctatttat tattatacat tgggattccg ttatattttt ctcctttcag 1785
ttcattttac ttcttaaaaa gtttcgttga tcgctattat gctatggatt caaagatttt 1845
ctttttctctc tcttcaaggt gtactctgca ttacggtttt ctttagttcg tttatttttt 1905
ttttgttaac aaggtgtttg tatacatata tataaatata tggaaatatt atagtgttta 1965
ttttgttact tcctgcgagt tgcaacagaa ctaacaagat gccatgctgt ttttttcat  2025
tttttggcta taaaaataac agtatcctag tccttgtgtt cggctttaaa atggaattgc 2085
aaacccccata attccttctt cacaccgaac aaaccgccta gtagtcgatt ttcagagact 2145
ctaatgcttt gaatataatt tttttcttca aaaatttcct taagcgtgct atcgaatgag 2205
tagacatcaa tcaagagttt catggtctcc ccgtatttgc cgctgcttct aatatttttg 2265
gagtgtagca tagcccaatc aatcaaatct tcgataatgc cactttttac atatacacga 2325
cgacaaccca cagtagtaac actcatgact aaattttcat cagtacttaa tgtcatgtta 2385
ggggctaacg aaatcaatgc aatgggcgtt tctctataaa cgatgatatg cgtattgttc 2445
accactggat cc                                                     2457
```

<210> 12
<211> 337
<212> PRT
<213> Saccharomyces cerevisiae

<400> 12
Met Lys Ile Ser Ala Ala Leu Ile Leu Ser Ser Leu Ser Ser Val Ala

```
 1                    5                    10                   15
Phe Ser Ala Pro Ala Pro Ala Pro Ala Asp Ser His His Glu Asp His
            20              25              30
His Lys Asp Glu Lys Pro Ala Val Val Thr Val Thr Gln Tyr Ile Asp
        35              40              45
Ser Asn Ala Ala Thr Ser Thr Val Glu Ser Ala Ala Thr Thr Thr Thr
        50              55              60
Leu Ser Ser Ser Glu Lys Asp Thr Ser Glu Gln Lys Arg Asp Gly Gly
65              70              75              80
Phe Gln Asp Gly Thr Val Lys Cys Ser Asp Phe Pro Ser Val Asn Gly
            85              90              95
Ile Val Ser Leu Asp Trp Leu Gly Phe Gly Gly Trp Ala Ser Val Met
            100             105             110
Asp Met Asp Ala Asn Thr Ser Ser Glu Cys Lys Asp Gly Tyr Tyr Cys
        115             120             125
Ser Tyr Ala Cys Glu Pro Gly Met Ser Lys Thr Gln Trp Pro Ser Asp
        130             135             140
Gln Pro Ser Asp Gly Lys Ser Val Gly Gly Leu Tyr Cys Lys Asn Gly
145             150             155             160
Tyr Leu Tyr Arg Thr Asn Thr Asp Thr Ser Asp Leu Cys Ser Thr Asp
            165             170             175
Glu Thr Ser Ala Lys Ala Ile Asn Lys Lys Ser Asp Ser Ile Ala Leu
            180             185             190
Cys Arg Thr Asp Tyr Pro Gly Ser Glu Asn Met Val Ile Pro Thr Val
        195             200             205
Val Asp Gly Gly Asp Ser Gln Pro Ile Ser Val Val Asp Glu Asp Thr
        210             215             220
Tyr Tyr Gln Trp Gln Gly Lys Lys Thr Ser Ala Gln Tyr Tyr Ile Asn
225             230             235             240
Asn Ala Gly Val Ser Ala Glu Asp Gly Cys Ile Trp Gly Thr Ser Gly
            245             250             255
Ser Asp Val Gly Asn Trp Ala Pro Leu Val Leu Gly Ala Gly Ser Thr
            260             265             270
Asn Gly Glu Thr Tyr Leu Ser Leu Ile Pro Asn Pro Asn Ser Asn Gln
        275             280             285
Ala Ala Asn Phe Asn Val Lys Ile Val Ala Ser Asp Gly Ala Asn Val
        290             295             300
Gln Gly Ser Cys Ala Tyr Glu Asp Gly Ser Phe Thr Gly Asp Gly Ser
305             310             315             320
Asp Gly Cys Thr Val Ser Val Leu Ser Gly Ser Ala Glu Phe Val Phe
            325             330             335
Tyr
```

<210> 13
<211> 2150
<212> DNA
<213> Saccharomyces cerevisiae

<220>
<221> CDS
<222> (563)...(1987)
<223> SAG1

<400> 13
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tgtttagtgc tacccaacta cttacattcc tttaaaaacc acaatattta agttaacctg 60
agctttattt ttagtaagtt atttaccaca atttttctca tacaccttta caatccgtat 120
tgccatgaat accaaggctt gctcagcttc tgcagcagtt caaccctttc caataccgcc 180
```

```
aatgcgtcct caaaacgtta gtttagtcgt gctcaaccgc tattttggt  tttatcttcg 240
tttcttctc  ctgaacgaca ttcgtcacga aaattgcggc ggaaaatttc ctgatgcgga 300
cactttttcc cgatccggac atgcctttt  ttggcgtttc gcgtcagtca atagaagttt 360
cagatctaca ttaggaagaa ccagaaaata gccattaatg ctttcagcat agcacagcat 420
agcagctgtg tatatcttaa ataagatgta gactggtttg catttggaaa ggttttgtgt 480
aagaaaagca atacttgagg taaaacaaga gaaaaaaaa  cactttacta actaatatcc 540
aatcctttat tttttgcag aa atg aaa ttc tca act gcc gtt act acg ttg 592
                        Met Lys Phe Ser Thr Ala Val Thr Thr Leu
                         1               5                    10
```

```
att agt tct ggt gcc atc gtg tct gct tta cca cac gtg gat gtt cac  640
Ile Ser Ser Gly Ala Ile Val Ser Ala Leu Pro His Val Asp Val His
                 15                  20                  25
```

```
caa gaa gat gcc cac caa cat aag agg gcc gtt gcg tac aaa tac gtt  688
Gln Glu Asp Ala His Gln His Lys Arg Ala Val Ala Tyr Lys Tyr Val
             30                  35                  40
```

```
tac gaa act gtt gtt gtc gat tct gat ggc cac act gta act cct gct  736
Tyr Glu Thr Val Val Val Asp Ser Asp Gly His Thr Val Thr Pro Ala
             45                  50                  55
```

```
gct tca gaa gtc gct act gct gct acc tct gct atc att aca aca tct  784
Ala Ser Glu Val Ala Thr Ala Ala Thr Ser Ala Ile Ile Thr Thr Ser
         60                  65                  70
```

```
gtg ttg gct cca acc tcc tcc gca gcc gct ggg ata gcc gct tcc att  832
Val Leu Ala Pro Thr Ser Ser Ala Ala Ala Gly Ile Ala Ala Ser Ile
 75                  80                  85                  90
```

```
gct gtt tca tct gct gcc tta gcc aag aat gag aaa atc tct gat gcc  880
Ala Val Ser Ser Ala Ala Leu Ala Lys Asn Glu Lys Ile Ser Asp Ala
                 95                  100                 105
```

```
gct gca tct gcc act gcc tca aca tct caa ggg gca tcc tcc tcc tcc  928
Ala Ala Ser Ala Thr Ala Ser Thr Ser Gln Gly Ala Ser Ser Ser Ser
             110                 115                 120
```

```
tcc tcc tcc tcg gca act tct acc cta gaa agc agc tct gtt tct tca  976
Ser Ser Ser Ser Ala Thr Ser Thr Leu Glu Ser Ser Ser Val Ser Ser
             125                 130                 135
```

```
tct agt gaa gaa gct gct cca aca tct act gtc gtg tca act tct tcc 1024
Ser Ser Glu Glu Ala Ala Pro Thr Ser Thr Val Val Ser Thr Ser Ser
     140                 145                 150
```

```
gca acc caa tct agt gct tct tct gcc act aaa tct agt act tct tcc 1072
Ala Thr Gln Ser Ser Ala Ser Ser Ala Thr Lys Ser Ser Thr Ser Ser
155                 160                 165                 170
```

```
act tca cca tct act tct act tct act tcc act tct tct act tcc tct 1120
Thr Ser Pro Ser Thr Ser Thr Ser Thr Ser Thr Ser Ser Thr Ser Ser
                 175                 180                 185
```

```
tcc tct tcc tcc tcc tcc tcc tct tct tct tct tct tct ggc agt ggt 1168
Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Gly Ser Gly
             190                 195                 200
```

```
agt atc tac ggt gat ttg gcc gac ttt tca ggc cca agt gag aaa ttc 1216
Ser Ile Tyr Gly Asp Leu Ala Asp Phe Ser Gly Pro Ser Glu Lys Phe
```

```
                 Ser Ile Tyr Gly Asp Leu Ala Asp Phe Ser Gly Pro Ser Glu Lys Phe
                     205                 210                 215

caa gac ggc act att cca tgt gac aaa ttc cca tct ggt caa ggt gtc       1264
Gln Asp Gly Thr Ile Pro Cys Asp Lys Phe Pro Ser Gly Gln Gly Val
    220                 225                 230

att tct att gac tgg att ggc gag ggt gga tgg tcc ggt gtg gaa aac       1312
Ile Ser Ile Asp Trp Ile Gly Glu Gly Gly Trp Ser Gly Val Glu Asn
235                 240                 245                 250

acc gac act tcc act ggc ggt tca tgc aag gag ggg tcc tac tgt tcc       1360
Thr Asp Thr Ser Thr Gly Gly Ser Cys Lys Glu Gly Ser Tyr Cys Ser
                255                 260                 265

tac tcc tgc caa cca ggt atg tct aag acc caa tgg cca tcc gat caa       1408
Tyr Ser Cys Gln Pro Gly Met Ser Lys Thr Gln Trp Pro Ser Asp Gln
                270                 275                 280

cca tct gac ggt aga tct gtc ggg ggt ttg ttg tgt aaa aat ggt tat       1456
Pro Ser Asp Gly Arg Ser Val Gly Gly Leu Leu Cys Lys Asn Gly Tyr
                285                 290                 295

ttg tac cgt tct aac act gac gcg gat tac tta tgt gaa tgg ggt gtc       1504
Leu Tyr Arg Ser Asn Thr Asp Ala Asp Tyr Leu Cys Glu Trp Gly Val
    300                 305                 310

gag gct gcc tat gtt gtt tct aaa cta agc aag ggt gtc gcc att tgc       1552
Glu Ala Ala Tyr Val Val Ser Lys Leu Ser Lys Gly Val Ala Ile Cys
315                 320                 325                 330

aga acc gac tac ccg ggc act gaa aac atg gtt atc cca acc tat gtt       1600
Arg Thr Asp Tyr Pro Gly Thr Glu Asn Met Val Ile Pro Thr Tyr Val
                335                 340                 345

gaa ggg ggt agc tct ttg cca ttg acc gtt gtt gac caa gat act tac       1648
Glu Gly Gly Ser Ser Leu Pro Leu Thr Val Val Asp Gln Asp Thr Tyr
                350                 355                 360

ttt act tgg gaa ggc aaa aag aca tct gct caa tac tac gtt aat aac       1696
Phe Thr Trp Glu Gly Lys Lys Thr Ser Ala Gln Tyr Tyr Val Asn Asn
                365                 370                 375

gcc ggc gtc tca gtt gaa gat ggg tgt atc tgg ggt act tct gga tct       1744
Ala Gly Val Ser Val Glu Asp Gly Cys Ile Trp Gly Thr Ser Gly Ser
    380                 385                 390

ggt att ggt aac tgg gca cca tta aac ttt ggt gct ggc tcc act ggt       1792
Gly Ile Gly Asn Trp Ala Pro Leu Asn Phe Gly Ala Gly Ser Thr Gly
395                 400                 405                 410

gga gtg aca tac tta tca ttg att cct aac cca aac aac agc gac gca       1840
Gly Val Thr Tyr Leu Ser Leu Ile Pro Asn Pro Asn Asn Ser Asp Ala
                415                 420                 425

ttg aac tac aac gtc aag ata gtt gct gct gat gat tca tcc aat gtc       1888
Leu Asn Tyr Asn Val Lys Ile Val Ala Ala Asp Asp Ser Ser Asn Val
                430                 435                 440
```

```
atc ggt gaa tgt gtt tac gaa aat ggt gag ttc tct ggc ggt gct gac   1936
Ile Gly Glu Cys Val Tyr Glu Asn Gly Glu Phe Ser Gly Gly Ala Asp
        445                 450                 455

ggg tgt acc gtc tct gtt act tcc ggt aaa gct cat ttc gtc tta tac   1984
Gly Cys Thr Val Ser Val Thr Ser Gly Lys Ala His Phe Val Leu Tyr
        460                 465                 470

aat taagctacgt gactactact tttccttttt tttttctttt ttcgaacaca        2037
Asn
475

tctcaccccc tatacctcac acaatcacta tggtcccctt ttctttttac cgatatttat 2097
actgtccacc tttttctttt cgttaatggc ctcaatgttt ctgtaccatt atc        2150
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<210> 14
<211> 475
<212> PRT
<213> Saccharomyces cerevisiae

<400> 14

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Met Lys Phe Ser Thr Ala Val Thr Thr Leu Ile Ser Ser Gly Ala Ile
1               5                   10                  15
Val Ser Ala Leu Pro His Val Asp Val His Gln Glu Asp Ala His Gln
            20                  25                  30
His Lys Arg Ala Val Ala Tyr Lys Tyr Val Tyr Glu Thr Val Val Val
        35                  40                  45
Asp Ser Asp Gly His Thr Val Thr Pro Ala Ala Ser Glu Val Ala Thr
    50                  55                  60
Ala Ala Thr Ser Ala Ile Ile Thr Thr Ser Val Leu Ala Pro Thr Ser
65                  70                  75                  80
Ser Ala Ala Ala Gly Ile Ala Ala Ser Ile Ala Val Ser Ser Ala Ala
                85                  90                  95
Leu Ala Lys Asn Glu Lys Ile Ser Asp Ala Ala Ala Ser Ala Thr Ala
            100                 105                 110
Ser Thr Ser Gln Gly Ala Ser Ser Ser Ser Ser Ser Ser Ser Ala Thr
        115                 120                 125
Ser Thr Leu Glu Ser Ser Ser Val Ser Ser Ser Ser Glu Glu Ala Ala
    130                 135                 140
Pro Thr Ser Thr Val Val Ser Thr Ser Ser Ala Thr Gln Ser Ser Ala
145                 150                 155                 160
Ser Ser Ala Thr Lys Ser Ser Thr Ser Ser Thr Ser Pro Ser Thr Ser
                165                 170                 175
Thr Ser Thr Ser Thr Ser Ser Thr Ser Ser Ser Ser Ser Ser Ser Ser
            180                 185                 190
Ser Ser Ser Ser Ser Ser Ser Gly Ser Gly Ser Ile Tyr Gly Asp Leu
        195                 200                 205
Ala Asp Phe Ser Gly Pro Ser Glu Lys Phe Gln Asp Gly Thr Ile Pro
    210                 215                 220
Cys Asp Lys Phe Pro Ser Gly Gln Gly Val Ile Ser Ile Asp Trp Ile
225                 230                 235                 240
Gly Glu Gly Gly Trp Ser Gly Val Glu Asn Thr Asp Thr Ser Thr Gly
                245                 250                 255
Gly Ser Cys Lys Glu Gly Ser Tyr Cys Ser Tyr Ser Cys Gln Pro Gly
            260                 265                 270
Met Ser Lys Thr Gln Trp Pro Ser Asp Gln Pro Ser Asp Gly Arg Ser
        275                 280                 285
Val Gly Gly Leu Leu Cys Lys Asn Gly Tyr Leu Tyr Arg Ser Asn Thr
    290                 295                 300
```

```
Asp Ala Asp Tyr Leu Cys Glu Trp Gly Val Glu Ala Ala Tyr Val Val
305             310             315                         320
Ser Lys Leu Ser Lys Gly Val Ala Ile Cys Arg Thr Asp Tyr Pro Gly
                325             330             335
Thr Glu Asn Met Val Ile Pro Thr Tyr Val Glu Gly Gly Ser Ser Leu
            340             345             350
Pro Leu Thr Val Val Asp Gln Asp Thr Tyr Phe Thr Trp Glu Gly Lys
        355             360             365
Lys Thr Ser Ala Gln Tyr Tyr Val Asn Asn Ala Gly Val Ser Val Glu
    370             375             380
Asp Gly Cys Ile Trp Gly Thr Ser Gly Ser Gly Ile Gly Asn Trp Ala
385             390             395                         400
Pro Leu Asn Phe Gly Ala Gly Ser Thr Gly Gly Val Thr Tyr Leu Ser
            405             410             415
Leu Ile Pro Asn Pro Asn Asn Ser Asp Ala Leu Asn Tyr Asn Val Lys
            420             425             430
Ile Val Ala Ala Asp Asp Ser Ser Asn Val Ile Gly Glu Cys Val Tyr
        435             440             445
Glu Asn Gly Glu Phe Ser Gly Gly Ala Asp Gly Cys Thr Val Ser Val
    450             455             460
Thr Ser Gly Lys Ala His Phe Val Leu Tyr Asn
465             470             475
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<210> 15
<211> 145
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> VARIANT
<222> (1)...(145)
<223> Xaa = Any Amino Acid

<400> 15
Thr Asp Tyr Pro Gly Xaa Glu Asn Met Val Xaa Pro Thr Xaa Val Xaa
  1             5               10              15
Xaa Gly Xaa Ser Xaa Pro Xaa Xaa Val Xaa Xaa Xaa Asp Xaa Tyr Xaa
            20              25              30
Xaa Trp Xaa Gly Lys Lys Thr Ser Ala Gln Tyr Tyr Xaa Asn Asn Xaa
        35              40              45
Gly Val Ser Xaa Glu Asp Gly Cys Ile Trp Gly Thr Xaa Gly Ser Xaa
    50              55              60
Xaa Gly Asn Trp Ala Pro Xaa Xaa Xaa Gly Ala Xaa Xaa Thr Xaa Gly
65              70              75                          80
Xaa Thr Tyr Leu Ser Xaa Ile Pro Asn Pro Asn Xaa Xaa Xaa Ala Xaa
            85              90                  95
Asn Xaa Asn Xaa Lys Ile Val Ala Xaa Asp Xaa Xaa Xaa Xaa Val Xaa
        100             105                 110
Gly Xaa Cys Xaa Tyr Glu Xaa Gly Xaa Xaa Xaa Gly Xaa Gly Xaa Asp
    115             120                 125
Gly Cys Thr Val Ser Val Xaa Ser Gly Xaa Ala Xaa Phe Val Xaa Tyr
    130             135                 140
Xaa
145
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<210> 16
<211> 60
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<212> PRT
<213> Saccharomyces cerevisiae

<400> 16
Ser Leu Ile Pro Asn Pro Asn Asn Gly Asn Ala Leu Asn Phe Asn Val
 1   5   10   15
Lys Ile Val Ala Ala Asp Asp Ser Ser Thr Val Asn Gly Glu Cys Ile
           20   25   30
Tyr Glu Asn Gly Ser Phe Ser Ser Gly Gly Ser Asp Gly Cys Thr Val
       35   40   45
Ser Val Thr Ala Gly Lys Ala Lys Phe Val Leu Tyr
    50   55   60

<210> 17
<211> 16
<212> PRT
<213> Saccharomyces cerevisiae

<400> 17
Leu Ala Thr Asp Gln Phe Gly Cys Arg Phe Leu Gln Lys Lys Leu Glu
 1   5   10   15

<210> 18
<211> 16
<212> PRT
<213> Saccharomyces cerevisiae

<400> 18
Leu Ile Leu Asp Pro Phe Gly Asn Tyr Leu Val Asp Lys Ile Cys Asp
 1   5   10   15

<210> 19
<211> 16
<212> PRT
<213> Saccharomyces cerevisiae

<400> 19
Ile Ser Ile Asn Gln Tyr Gly Thr Arg Ser Leu Gln Lys Ile Ile Asp
 1   5   10   15

<210> 20
<211> 15
<212> PRT
<213> Saccharomyces cerevisiae

<400> 20
Leu Ile Asn Asp Ile Asn Gly His Val Ile Gln Lys Cys Ile Phe
 1   5   10   15

<210> 21
<211> 16
<212> PRT
<213> Saccharomyces cerevisiae

<400> 21
Ile Ser Thr His Lys His Gly Cys Cys Val Leu Gln Lys Ile Leu Ser
1   5   10   15

<210> 22
<211> 16
<212> PRT
<213> Saccharomyces cerevisiae

<400> 22
Leu Ile Asn Asp Gln Phe Gly Asn Tyr Ile Ile Gln Phe Ile Leu Asp
1   5   10   15

<210> 23
<211> 16
<212> PRT
<213> Saccharomyces cerevisiae

<400> 23
Leu Ser Cys Leu Lys Phe Ser Ser Asn Val Val Glu Lys Phe Ile Lys
1   5   10   15

<210> 24
<211> 16
<212> PRT
<213> Saccharomyces cerevisiae

<400> 24
Leu Ile Arg Asp Asn Phe Gly Asn Tyr Ala Leu Gln Thr Leu Leu Asp
1   5   10   15

<210> 25
<211> 16
<212> PRT
<213> Saccharomyces cerevisiae

<400> 25
Leu Cys Lys Asp Gln His Gly Cys Arg Phe Leu Gln Lys Gln Leu Asp
1   5   10   15

<210> 26
<211> 16
<212> PRT
<213> Saccharomyces cerevisiae

<400> 26
Leu Met Thr Asp Ser Phe Gly Asn Tyr Leu Ile Gln Lys Leu Leu Glu
1   5   10   15

<210> 27
<211> 16
<212> PRT
<213> Saccharomyces cerevisiae

<400> 27
Ile Ser Leu Asn Pro His Gly Thr Arg Ala Leu Gln Lys Leu Ile Glu
1   5   10   15

<210> 28
<211> 16
<212> PRT
<213> Saccharomyces cerevisiae

<400> 28
Leu Ser Lys Asp Leu Asn Gly Asn His Val Ile Gln Lys Cys Leu Gln
1   5   10   15

<210> 29
<211> 16
<212> PRT
<213> Saccharomyces cerevisiae

<400> 29
Ile Ala Thr His Arg His Gly Cys Cys Val Leu Gln Arg Cys Leu Asp
1   5   10   15

<210> 30
<211> 16
<212> PRT
<213> Saccharomyces cerevisiae

<400> 30
Leu Thr Leu Asp Pro Phe Gly Asn Tyr Val Val Gln Tyr Ile Ile Thr
1   5   10   15

<210> 31
<211> 16
<212> PRT
<213> Saccharomyces cerevisiae

<400> 31
Leu Ser Ile His Lys Phe Gly Ser Asn Val Ile Glu Lys Ile Ile Lys
1   5   10   15

<210> 32
<211> 16
<212> PRT
<213> Saccharomyces cerevisiae

<400> 32
Leu Leu Asn Asp Ser Tyr Gly Asn Tyr Val Leu Gln Thr Ala Leu Asp
1   5   10   15

<210> 33
<211> 16
<212> PRT
<213> Drosophila

<400> 33
Phe Ser Gln Asp Gln His Gly Ser Arg Phe Ile Gln Gln Lys Leu Glu
 1   5   10   15

<210> 34
<211> 16
<212> PRT
<213> Drosophila

<400> 34
Leu Met Thr Asp Val Phe Gly Asn Tyr Val Ile Gln Lys Phe Phe Glu
 1   5   10   15

<210> 35
<211> 16
<212> PRT
<213> Drosophila

<400> 35
Leu Ala Leu Gln Met Tyr Gly Leu Arg Val Ile Gln Lys Ala Leu Glu
 1   5   10   15

<210> 36
<211> 16
<212> PRT
<213> Drosophila

<400> 36
Cys Val Lys Asp Gln Asn Gly Asn His Val Val Gln Lys Cys Ile Glu
 1   5   10   15

<210> 37
<211> 16
<212> PRT
<213> Drosophila

<400> 37
Leu Ser Thr His Pro Tyr Gly Cys Arg Val Ile Gln Arg Ile Leu Glu
 1   5   10   15

<210> 38
<211> 16
<212> PRT
<213> Drosophila

<400> 38
Leu Ile Gln Asp Gln Tyr Gly Asn Tyr Val Ile Gln His Val Leu Glu
 1   5   10   15

<210> 39
<211> 16
<212> PRT
<213> Drosophila

<400> 39
Leu Ser Gln His Lys Phe Ala Ser Asn Val Val Glu Lys Cys Val Thr
1   5   10   15

<210> 40
<211> 16
<212> PRT
<213> Drosophila

<400> 40
Met Met Lys Asp Gln Tyr Ala Asn Tyr Val Val Gln Lys Met Ile Asp
1   5   10   15

<210> 41
<211> 16
<212> PRT
<213> Homo sapiens

<400> 41
Phe Ser Gln Asp Gln His Gly Ser Arg Phe Ile Gln Leu Lys Leu Glu
1   5   10   15

<210> 42
<211> 16
<212> PRT
<213> Homo sapiens

<400> 42
Leu Met Arg Asp Val Phe Gly Asn Tyr Val Ile Gln Lys Phe Phe Glu
1   5   10   15

<210> 43
<211> 16
<212> PRT
<213> Homo sapiens

<400> 43
Leu Ala Leu Gln Met Tyr Gly Leu Arg Val Ile Gln Lys Ala Leu Glu
1   5   10   15

<210> 44
<211> 16
<212> PRT
<213> Homo sapiens

<400> 44
Cys Val Lys Asp Gln Asn Gly Asn His Val Val Gln Lys Cys Ile Glu
1   5   10   15

<210> 45
<211> 16
<212> PRT
<213> Homo sapiens

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<400> 45
Leu Ser Thr His Pro Tyr Gly Cys Arg Val Ile Gln Arg Ile Leu Glu
 1               5                  10                  15


<210> 46
<211> 16
<212> PRT
<213> Homo sapiens

<400> 46
Leu Val Gln Asp Gln Tyr Gly Asn Tyr Val Ile Gln His Val Leu Glu
 1               5                  10                  15


<210> 47
<211> 16
<212> PRT
<213> Homo sapiens

<400> 47
Val Leu Ser Gln His Phe Ala Ser Asn Val Val Glu Lys Cys Val Thr
 1               5                  10                  15


<210> 48
<211> 16
<212> PRT
<213> Homo sapiens

<400> 48
Met Met Lys Asp Gln Tyr Ala Asn Tyr Val Val Gln Lys Met Ile Asp
 1               5                  10                  15
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